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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND BT 474 CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human BT 474 cells is described. Also described are single exon nucleic acid probes expressed in the BT 474 cells and their use in methods for detecting gene expression.

WO 01/57271 A2



HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND BT 474 CELLS

5 CROSS REFERENCE TO RELATED APPLICATIONS

The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the  
10 benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of  
15 UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY

20 REFERENCE THEREOF

The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in  
25 triplicate, containing a file named pto\_BT474.txt, created 24 January 2001, having 11,325,593 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

30 Field of the Invention

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In  
35 particular, the present invention relates to unique genome-

derived single exon nucleic acid probes expressed in human BT 474 cells and single exon nucleic acid microarrays that include such probes.

## 5 Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4  
10 (1973), these techniques were used principally as tools to further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had  
15 been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane  
20 association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

25 More recently, however, the development of high throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes  
30 understanding of the basic biology of the encoded protein product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of  
35 mRNA – are of greatest initial interest. This "expressed

sequence tag" ("EST") approach has already yielded vast amounts of sequence data (see for example Adams et al., *Science* 252:1651 (1991); Williamson, *Drug Discov. Today* 4:115 (1999)). For nucleic acids sequenced by this approach, often the only biological information that is known *a priori* with any certainty is the likelihood of biologic expression itself. By virtue of the species and tissue from which the mRNA had originally been obtained, most such sequences are also annotated with the identity of the species and at least one tissue in which expression appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot be presumed; often the only *a priori* biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing approaches - and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species - there is an increasing need for methods that rapidly and effectively permit the functions of nucleic sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, *Science* 280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),



there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears  
5 the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found  
10 by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST  
15 sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of  
20 the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and  
25 most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function  
30 difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al.,  
35 *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et

al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,  
*Ismb* 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol.*  
*Biol.* 268:78-94 (1997), predict many putative genes without  
known homology or function. Such programs are known,  
5 however, to give high false positive rates. Burset et al.,  
*Genomics* 34:353-367 (1996). Using a consensus obtained by  
a plurality of such programs is known to increase the  
reliability of calling exons from genomic sequence.  
Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

10 Identification of functional genes from genomic  
data remains, however, an imperfect art. For example, in  
reporting the full sequence of human chromosome 21, the  
Chromosome 21 Mapping and Sequencing Consortium reports  
that prior bioinformatic estimates of human gene number may  
15 need to be revised substantially downwards. *Nature*  
405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus  
that permit the functions of the regions identified  
bioinformatically — and specifically, that permit the  
20 expression of regions predicted to encode protein — readily  
to be confirmed experimentally.

Recently, the development of nucleic acid  
microarrays has made possible the automated and highly  
parallel measurement of gene expression. Reviewed in  
25 Schena (ed.), DNA Microarrays : A Practical Approach  
(Practical Approach Series), Oxford University Press (1999)  
(ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60  
(1999); Schena (ed.), Microarray Biochip: Tools and  
Technology, Eaton Publishing Company/BioTechniques Books  
30 Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from  
cDNA/EST libraries, either from those previously described  
in the literature, such as those from the I.M.A.G.E.  
consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or  
35 from the construction of "problem specific" libraries

targeted at a particular biological question, R.S. Thomas  
et al., *Cancer Res.* (in press). Such microarrays by  
definition can measure expression only of those genes found  
in EST libraries, and thus have not been useful as probes  
5 for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid  
microarrays to answer certain biological questions has been  
demonstrated for the yeast *Saccharomyces cerevisiae*. De  
Risi et al., *Science* 278:680 (1997). The vast majority of  
10 yeast nuclear genes, approximately 95% however, are single  
exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-  
1137 (1999); Goffeau et al., *Science* 274:563-67 (1996),  
permitting coding regions more readily to be identified.  
Whole genome nucleic acid microarrays have not generally  
15 been used to probe gene expression from more complex  
eukaryotic genomes, and in particular from those averaging  
more than one intron per gene.

Diseases of the breast are a significant cause of  
human morbidity and mortality. Increasingly, genetic  
20 factors are being found that contribute to predisposition,  
onset, and/or aggressiveness of most, if not all, of these  
diseases. Although mutations in single genes have been  
identified as causative for some diseases of the breast,  
for the most part these disorders are believed to have  
25 polygenic etiologies. There is a need for methods and  
apparatus that permit prediction, diagnosis and prognosis  
of diseases of the human breast, particularly those  
diseases with polygenic etiology.

### 30 Summary of the Invention

The present invention solves these and other  
problems in the art by providing methods and apparatus for  
predicting, confirming, and displaying functional  
35 information derived from genomic sequence. The present

invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel  
5 genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids  
10 identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single  
15 exon nucleic acid probes for measuring gene expression in a sample derived from human breast, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 5,205 or a complementary sequence, or a portion of such a sequence.

20 By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably  
25 amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality  
30 of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000  
35 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 10,317 or a complimentary sequence, or a  
5 portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp,  
10 preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least  
15 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is  
20 preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

25 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane  
30 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene,  
35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

5 In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

10 In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

15 In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of  
20 SEQ ID Nos. 5,206 - 10,317, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 5,205.

25 Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human breast which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 -  
30 5,205 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human breast.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a  
35 nucleotide sequence as set out in any of SEQ ID NOs.: 5,206

- 10,317 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human breast which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 10,318 - 15,438 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human breast.

10 Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15,  
15 suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth  
20 aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

25 Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or  
30 fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3  
35 and Cy5 although other suitable dyes will be known to those

skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human Breast, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human Breast; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the Breast of said eukaryote, said



probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

10 identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 10,317 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 5,206 - 10,317, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -5,205.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 10,318 - 15,438.

Accordingly in a eleventh aspect of the invention

there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 10,318 - 15,438, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

### Detailed Description of the Invention

#### 15 Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., Proc. Natl. Acad. Sci. USA 97(4):166501670 (2000);

in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO.; the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a

sequence of amino acids. The sequences referred to as  
PEPTIDE SEQ ID NOS.: are the predicted peptide sequences  
that would be translated from one of the exons, or a  
portion thereof set out in exon SEQ ID NOS.:.. The codons  
5 encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined  
nucleotide sequence or sequences can be and, preferably,  
are fragments unique to that sequence or to one or a  
combination of those sequences. A fragment unique to a  
10 nucleic acid molecule is one that is a signature for the  
larger nucleic acid molecule.

As used herein, the phrase "expression of a  
probe" and its linguistic variants means that the ORF  
present within the probe, or its complement, is present  
15 within a target mRNA.

As used herein, "stringent conditions" refers to  
parameters well known to those skilled in the art. When a  
nucleic acid molecule is said to be hybridisable to another  
of a given sequence under "stringent conditions" it is  
20 meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding  
pair" intends a pair of molecules that bind to one another  
with high specificity. Binding pairs are said to exhibit  
specific binding when they exhibit avidity of at least  $10^7$ ,  
25 preferably at least  $10^8$ , more preferably at least  $10^9$   
liters/mole. Nonlimiting examples of specific binding  
pairs are: antibody and antigen; biotin and avidin; and  
biotin and streptavidin.

As used herein with respect to the visual display  
30 of annotated genomic sequence, the term "rectangle" means  
any geometric shape that has at least a first and a second  
border, wherein the first and second borders each are  
capable of mapping uniquely to a point of another visual  
object of the display.

35 As used herein, a "Mondrian" means a visual

display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

5

#### Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and  
10 examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in  
15 meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

20 FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length  
25 shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color  
30 hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

35 FIG. 7 is a pictorial representation of the

expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured  
5 tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

10 FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a  
15 BLAST Expect ("E") value of greater than  $1e-30$  ( $1 \times 10^{-30}$ ) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than  $1e-30$  ( $1 \times 10^{-30}$ ) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases  
20 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

25 Methods and Apparatus for Predicting, Confirming,  
Annotating, and Displaying Functional Regions From Genomic  
Sequence Data

FIG. 1 is a flow chart illustrating in broad  
30 outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original  
35 sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than

human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

5           Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to,  
10   encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing  
15   somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

          The particular genomic sequence to be input into process 200 will depend upon the function for which  
20   relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

25           Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic  
30   assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

35           The subset of sequences output from process 300



is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

5           Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by  
10 incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for  
15 incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process  
20 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output  
25 from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational  
30 substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.  
35 Often, data will be stored after each, or at least a

plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently  
5 long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment  
10 length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal  
15 number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes  
20 (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate  
25 a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been  
30 described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is  
35 possible to query the database for newly added sequence,

either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired

analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as  
5 processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis.

10 Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

15 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using  
20 programs well known in the art, such as CROSS\_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified  
25 algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can  
30 be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the  
35 undesired sequence as, for example, by converting the

specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after

transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase  
5 reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

10 Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to  
15 process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report  
20 consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7%  
25 of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

30 Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process  
35 can be repeated on the same input sequence, or subset



thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based inter alia upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully

to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that  
5 subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message,  
10 reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

15 The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

20 As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The  
25 combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In  
30 particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

35 Putative ORFs as predicted by a consensus of gene

calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is  
5 conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic)  
10 sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500  
15 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more  
20 effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400  
25 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs  
30 predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at  
35 amplifying pieces of such ORFs is low, and that such

putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been

obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology  
5 : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4<sup>th</sup> edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2<sup>nd</sup> edition (December 1989), Cold Spring Harbor Laboratory  
10 Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material  
15 flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the  
20 absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial  
25 advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support  
30 substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

35 Typically, the support substrate will be glass,

although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, .  
5 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even  
10 spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached  
15 covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

20 Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources  
25 (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays  
30 typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or  
35 32 *E. coli* genes suffice to provide a robust measure of

background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural  
5 nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the  
10 immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates,  
15 the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

20 For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using  
25 nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid  
30 probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For  
35 example, each standard microscope slide can include at

least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

5           Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as  
10 is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

          The genome-derived single exon microarrays  
15 described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3)  
20 those constructed from yeast genomic DNA.

          Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above,  
25 it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question,  
30 R.S. Thomas et al., Cancer Res. (in press). Such microarrays are herein collectively denominated "EST microarrays".

          Such EST microarrays by definition can measure expression only of those genes found in EST libraries,  
35 shown herein to represent only a fraction of expressed



genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message  
5 successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression  
10 measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences  
15 that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription,  
20 optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor  
25 cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from  
30 genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST  
35 approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

5           As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a  
10 spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

          In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention  
15 lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T,  
20 where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

          A further distinction, which also affects the specificity of hybridization, is occasioned by the typical  
25 derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the  
30 probes are amplified, rather than excised, from the vector.

          In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from  
35 genomic DNA. Typically, therefore, at least about 50, 60,

70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage.

5 Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including

10 probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

15 As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes

20 disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific

25 primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the

30 genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even

35 smaller amount of nonspecific sequence that would

contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the

probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the

present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

5           Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization  
10 results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

          In contrast, the longer probe length of the  
15 genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or  
20 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

25           A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound  
30 noncovalently to the substrate.

          Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large  
35 percentage differences in the theoretically optimum

stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari *et al.*, *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez *et al.*, *Nucl. Acids Res.* 28:85-86 (2000); Spingola *et al.*, *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred

embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the



reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes  
5 prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned  
10 using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the  
15 genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for  
20 subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention  
25 provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is  
30 disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher  
35 density arrays, such as are provided by microtiter plates

having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-  
5 noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each  
10 probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second,  
15 different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be  
20 packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a  
25 genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the  
30 genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation  
35 information, such as gene expression data. Such recordable

media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then  
5 separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should  
10 be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and  
15 characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic  
20 sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected  
25 of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,  
30 SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query -  
35 including information on identical sequences and

information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, 5 process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such 10 annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or 15 by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

20 The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the 25 information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively 30 described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an 35 annotated sequence, representation of individual

nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention  
5 herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian  
10 visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of  
15 rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically -- for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 -- or through user intervention,  
20 as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession  
25 number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is  
30 anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual  
35 display 80 is used as a graphical user interface to

computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

5           Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle  
10 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

          Where a single bioinformatic method or approach  
15 identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of  
20 horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

          Thus, rectangles 83a in FIG. 3 represent the  
25 functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or  
30 approach.

          Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from  
35 GRAIL or GRAIL II, rectangles 83b can represent the results

from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such

display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of



bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as

can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of  
5 expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which  
10 often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right  
15 borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical  
20 assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays,  
25 individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the  
30 spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such  
35 relative expression (expression ratios) and absolute

expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

### 30 Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present

invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of  
5 single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present  
10 invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example  
15 readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 5,205 of these ORFs in BT 474 cells.

20 The BT474 cell line is a human mammary ductal carcinoma cell line that is tumorigenic in nude mice. It was isolated from a solid, invasive ductal carcinoma of the breast, Lasfargues et al., J. Natl Cancer Inst. 61(4):967-78 (1978), and is epithelial and neoplastic. The cell line  
25 grows as adherent patches of epithelial cells with compact, multilayered colonies, rarely become confluent.

The cell line is aneuploid human female (XO usually), with most chromosome counts in the hypertetraploid range. Several chromosomes (N11, N13, and N22) are absent, and  
30 others are clearly under-represented (N9, N14, and N15) with respect to the other normal chromosomes. Chromosome N7 tends towards over-representation in several karyotypes. Some of the missing normal chromosomes are represented by their involvement in the nine stable marker chromosomes.

35 As would immediately be appreciated by one of skill in

the art, each single exon probe having demonstrable expression in BT 474 cells is currently available for use in measuring the level of its ORF's expression in breast cells.

5 Diseases of the breast are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been  
10 identified as causative for some diseases of the breast, for the most part these disorders are believed to have polygenic etiologies.

For example, according to the American Cancer Society (ACS), carcinoma of the breast is the second most  
15 common cancer in women and, after lung cancer, is the second deadliest. The ACS estimates that in the U.S. there occurred 182,800 new cases of malignant breast cancer in 2000, and about 40,800 deaths from the disease. Although incidence of breast cancer is said to have declined, the  
20 disease clearly continues to represent a serious risk to the health and life of American women. Indeed, about one in nine U.S. women will develop breast cancer in her lifetime, and at present mortality rates, about a third of such women will eventually die from the disease.

25 A variety of factors are known to increase the risk of breast carcinoma. Sex is one: breast cancer in men is rare. Age is another: as women age, their risk for developing breast cancer increases, a 70 year old woman having three times the risk of developing cancer and five  
30 times the risk of dying from the disease as compared to a 40 year old woman. Most breast cancers occur after age 50, although in women with a genetic susceptibility, breast cancer tends to occur at an earlier age than in sporadic cases. Reproductive and menstrual history are also known  
35 to affect risk, with risk increasing with early menarche

and late menopause, and is reduced by early first full term pregnancy. Additional risk factors, oft-times termed "lifestyle factors", include weight gain, obesity, fat intake, alcohol consumption, and level of physical  
5 activity.

That genetic factors underlie the etiology of breast cancer is suggested by the approximately two-fold increased risk for development of breast cancer by women with a first-degree relative who has also developed breast  
10 cancer. After gender and age, a positive family history is the strongest known predictive risk factor for breast cancer. Genetic linkage analysis in families with high rates of inherited cancer have facilitated the identification of several genes in which mutations can be  
15 shown to contribute substantially to the development and progression of breast cancer, including BRCA1, BRCA2, p53, and PTEN/MMAC1. Further study has made clear, however, that these genes are not alone sufficient to explain all genetic contributions to breast cancer.

20 For example, BRCA1 appears to be responsible for disease in up to 90% of families with both breast and ovarian cancer, but in only 45% of families with multiple cases of breast cancer without occurrence of ovarian cancer. And mutations in BRCA2, localized to the long arm  
25 of chromosome 13, are thought to account for only approximately 35% of multiple case breast cancer families. Furthermore, despite the strong correlation between germline mutations in BRCA1 or BRCA2 and development of breast cancer, only weak connections have been made between  
30 these genes and sporadic breast cancer.

Epistatic effects of BRCA1 and BRCA2 mutations on other genetic loci, only some of which have been identified, have been postulated to account for some of the deleterious effects of mutations in these two genes.

35 Thus, mutations in p53 seem to be much more

frequent in BRCA1 breast cancers (20/26) and somewhat more frequent in BRCA2-associated breast cancers (10/22) than in grade-matched sporadic cancers (7/20). BRCA mutation-associated cancers contain p53 mutations not typically found in sporadic breast cancer, and 12 individual hereditary breast cancers have been shown to contain more than a single p53 mutation. Mutations of BRCA1 and BRCA2 may thus confer a "mutator" phenotype permitting the accumulation of genetic abnormalities, with p53 inactivation selected during tumor progression.

Additionally, genome-wide screening for chromosomal gains or losses in breast cancers harboring BRCA1 or BRCA2 mutations demonstrated more regions that were amplified or deleted compared to controls, suggesting a generalized increase in large-scale genomic instability. Chromosomes 5q, 4q, and 4p had very frequent loss of heterozygosity in BRCA1 tumors, while BRCA2 tumors were characterized by losses at 13q (near the BRCA2 locus itself) and 6q, and chromosomal gains at 17q (outside of the HER2/neu locus) and 20q.

Mutations of other genes have also been implicated in susceptibility to development or aggressiveness of breast cancer. For example, germline mutations in the ATM gene, localized to chromosome 11q22-23, result in an increased risk of breast cancer among female heterozygote carriers with an estimated relative risk of 3.9 to 6.4; it is unclear, however, if mutations in the ATM gene itself contribute to breast cancer.

Normal allelic variation in a variety of genes, as opposed to frank mutation, may also influence susceptibility to developing breast carcinoma and the propensity for the disease to progress. Such polymorphisms may thus explain why particular women or ethnic groups who do not otherwise bear mutations in genes

known to be linked to breast cancer are at greater risk, especially in the context of exposure to environmental agents and other nonhereditary risk factors.

Polymorphically expressed genes may code for enzymes that  
5 metabolize estrogens or detoxify drugs and environmental carcinogens.

For example, molecular epidemiologic studies of cancer of the breast have examined associations with p450 cytochrome genotypes including CYP1A1, CYP2D6, and CYP17.

10 The CYP1A1 gene, located on chromosome 15q, encodes the enzyme aryl hydrocarbon hydroxylase (AHH), present in breast tissue, and which catabolizes polycyclic aromatic hydrocarbons and arylamines. AHH is strongly inducible, i.e., greater enzymatic activity is seen with greater  
15 exposure to substrates. AHH catalyzes the monooxygenation of polycyclic aromatic hydrocarbons to phenolic products and epoxides that may be carcinogenic. AHH is also involved in the conversion of estrogen to hydroxylated conjugated estrogens such as 2-hydroxyestradiol.

20 Three polymorphisms in the CYP1A1 gene have been identified: an MspI RFLP of the 3' end of the gene (MspI); an adenine to guanine mutation in exon 7, causing an isoleucine to valine substitution (Ile-Val); and a polymorphism of the CYP1A1 gene identified among Negroids.  
25 The frequencies of the MspI and Ile-Val polymorphisms vary considerably by race, being higher among Japanese and Hawaiian populations as compared with Caucasians and Negroids.

The CYP2D6 gene is located on chromosome 22q and  
30 encodes the enzyme debrisoquine hydroxylase, which metabolizes a variety of drugs and other xenobiotics. Like other polymorphically expressed p450 enzymes, it may activate procarcinogens or, conversely, detoxify carcinogens. A number of alleles have been characterized  
35 at the CYP2D6 locus. The "poor metabolizer" phenotype



(CYP2D6 mutant/mutant genotype), which is rare in Asians, occurs in about 5% to 10% of Caucasians and in 2% of Negroids.

As another example, the N-acetyl transferase-1 (NAT1) and N-acetyl transferase-2 (NAT2) genes are located on chromosome 8q. Allelic variation in the NAT genes may contribute to variation in populations as to the susceptibility of individuals to development of breast carcinoma, particularly in the context of exposure to compounds present in tobacco. NAT2 detoxifies or, conversely, activates aromatic amines found in tobacco smoke such as 4-aminobiphenyl. Both phenotypic assays and genotypic assays for NAT2 can be used to classify individuals as rapid or slow acetylators. Genetic variants of the NAT2 gene have been cloned and 6 alleles at this locus have been identified: the F1 allele confers the fast acetylator phenotype. The distribution of NAT1 and NAT2 alleles differs widely between racial and ethnic groups.

As yet another example, the glutathione S-transferase-M1 (GSTM1) gene is located on chromosome 1 and the gene for glutathione S-transferase-T1 (GSTT1) is located on chromosome 11q. A glutathione S-transferase-P1 (GSTP1) gene has also been identified. Glutathione S-transferases detoxify a variety of carcinogens and cytotoxic drugs (for example, benzo(a)pyrene, monohalomethanes such as methyl chloride, ethylene oxide, pesticides, and solvents used in industry) by catalyzing the conjugation of a glutathione moiety to the substrate. Allelic variation in the glutathione-S-transferase genes may contribute to variation in populations as to the susceptibility of individuals to development of breast carcinoma, particularly in the context of exposure to environmental toxins. Individuals homozygous for deletions in the GSTM1, GSTT1, or GSTP1 genes may have a higher risk of cancer of the breast and

other sites because of their impaired ability to metabolize and eliminate carcinogens.

GSTM1 is polymorphically expressed and 3 alleles at the GSTM1 locus have been identified: GSTM1-0 (homozygous deletion genotype), GSTM1a, and GSTM1b. The null allele (GSTM1-0) is present in about 38% to 67% of Caucasians and 22% to 35% of Negroids. GSTM is not expressed in breast tissue at high levels. Two functionally different genotypes at the GSTT1 locus have been described: GSTT1-0 (homozygous deletion genotype) and GSTT1-1 (genotypes with 1 or 2 undeleted alleles). A polymorphism of the GSTP1 gene, A313G (changing codon 105 from Ile to Val), has been identified. The GSTT1-0 allele has been associated with accelerated age of first breast cancer diagnosis as compared with the GSTT1-1 allele.

Many other genes have been suggested to be involved in the development and/or progression of breast cancer, either as a result of gain of function or loss of function mutations, or as a result of normal allelic variation within different populations. A nonexhaustive list of such genes, each followed by the gene's chromosomal location, if known, follows: AMPH 7p14-p13; AMPHL (BIN1, SH3P9) 2q14; API4 (survivin, SVV) 17q25(?); ARHA (ARH12, RhoA) 3p21.3; ARHC (RhoC) 1p21-p13; ATM (ATA, ATC) 11q22.3; BAG1 9p12; BARD1 2q34-q35; BCAR1 16q23.1; BCAR2; BCAR3 (NSP2); BCAS1 (NABC1, AIBC1) 20q13.2-q13.3; BRCA1 17q21; BRCA2 13q12.3; CCND1 (D11S287E, Cyclin D, PRAD1) 11q13; CD44 (MDU3, HA, MDU2) 11pter-p13; CD9 (p24, MIC3, BA2) 12p13; CDKN1B (KIP1, P27) 12p13; CDKN2A (P16, INK4A, MTS1) 9p21; COMT 22q11.2; COT (MAP3K8, TPL-2, EST) 10p11.2; CSK (c-src) 15q23-q25; CTSD (CPSD) 11p15.5; CYP17 10q24.3; CYP19 15q21.1; CYP1A1 (CYP1) 15q22-q24; CYP1B1 (GLC3A) 2p22-p21; EFNB2 (EPLG5, LERK5, ephrin-B2) 13q33; EIF3S6 (INT6) 8q22-q23; EIF4E (EIF-4E) 4q21-q25; EMS1 11q13; ERBB2 (HER2, NEU) 17q11.2-q12; ERBB3 (HER3) 12q13; ESR1 (ESRA)

6q25.1; ESR2 (ESRB, ERBeta) 14q; FGF8 (AIGF)  
 10q24; GSTM1 (GST1, MU) 1p13.3; GSTP1 (FAEES3, GST3, PI)  
 11q13; GSTT1 22q11.23; HRAS 11p15.5; HSPB1 (HSP27) 7q;  
 HSPCA (HSP90A , HSPC1); HSPCB (HSP90B, HSPC2) 6p12; IGF1  
 5 12q22-q24.1; IGF1R (JTK13) 15q25-q26; IGF2 11p15.5; IL6  
 (IFNB2) 7p21; ING1 13q34; KISS1 (KiSS-1) 1q32; KLK3 (PSA,  
 APS) 19q13; LASP1 (MLN50) 17q11-q21.3; LIBC 6q22; MAP2K4  
 (MKK4, SEK1, JNKK1) 17p11.2; MKI67 (Ki-67) 10q25-qter;  
 MMP11 (STMY3, STR3) 22q11.2; MMP2 (CLG4A, CLG4, GELA)  
 10 16q13; MUC1 (PUM, PEM) 1q21; MYC (CMYC, C-MYC) 8q24.12-  
 q24.13; NOTCH4 (INT3, NOTCH3) 6p21.3; PCNA 20p12; PI5  
 (maspin ) 18q21.3; PLAUI (uPA , URK) 10q24; PSEN2 (D21S21,  
 HPS2, BCEI) 21q22.3; RARB (NR1B2, HAP) 3p24; RB1 (Rb)  
 13q14.2; S100A4 (MTS1, P9KA, metastasin) 1q21; SLC22A1L  
 15 (BWSCR1A, ORCTL2, IMPT1) 11p15.5; SNCG (BCSG1) 10q23.2-  
 q23.3; SRD5A2 2p23; STIP1 (HSP70) 11?; STK11 (LKB1, PJS)  
 19p13.3; TFAP2A (AP2 , AP2TF) 6p24; TFAP2B (AP2B) 6p12;  
 TFAP2C 20q13.2; TFF1 (D21S21, BCEI) 21q22.3; TGFBR2 3p22;  
 TIMP2 17q25; TP53 (p53 , P53) 17q13.1; TPD52 (D52) 8q21;  
 20 TPD52L1 (D53, hD53) 6q22-q23; TSG101 11p15.2-p15.1.

The etiology of non-cancerous disorders of the breast may also involve genetic factors. Such disorders include disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast  
 25 disease, and non-carcinoma tumors.

Disorders of development of the breast include supernumerary nipples or breasts; accessory axillary breast tissue; congenital inversion of the nipples; and macromastia.

30 Inflammatory diseases of the breast include acute mastitis; periductal mastitis, also called recurrent subareolar abscess and squamous metaplasia of the lactiferous ducts; mammary duct ectasia; fat necrosis; and granulomatous mastitis, including granulomatous lobular  
 35 mastitis. Systemic granulomatous diseases that can affect

the breast include Wegener granulomatosis and sarcoidosis.

Proliferative breast diseases include epithelial hyperplasia; sclerosing adenosis; and small duct papillomas. Non-carcinoma tumors include stomal tumors including fibroadenoma and phyllodes tumor, and sarcomas that include angiosarcoma, rhabdomyosarcoma, liposarcoma, leiomyosarcoma, chondrosarcoma and osteosarcoma. Other breast tumors include epithelial cell tumors including large duct papillomas.

10           The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human breast, particularly those diseases with polygenic etiology. With each of the single  
15 exon probes described herein shown to be expressed at detectable levels in human breast cancer cells, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

20           For example, diagnosis, grading, and/or staging of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of a given breast disease, or to specific grades or stages  
25 thereof.

          In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the patient's breast to the genome-derived single exon  
30 microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed

in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of breast disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human breast. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the BT 474 cells has been demonstrated are useful for both measurement in the breast and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was

measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

5           Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

10           The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

15           Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

20           Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999);

35           Voehringer et al., "Gene Microarray Identification of Redox

and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine  
5 abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,  
10 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and  
15 Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the  
20 Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

25 In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change,  
30 serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway  
35 of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in BT 474 cells.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates,



morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe

composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 5,206 - 10,317, respectively, for probe SEQ ID NOS. 1 - 5,205. The minimum amount of ORF required to be included in the probe of the present invention in order to

provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 5,206 - 10,317 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c<sub>ot</sub>1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more

than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly  
5 translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further  
10 be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have  
15 sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or  
20 both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution  
25 hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as  $^3\text{H}$ ,  $^{32}\text{P}$ ,  $^{33}\text{P}$ ,  $^{35}\text{S}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR<sup>®</sup>

30 Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or  
35 enhanced chemiluminescent detection; labels suitable for

ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human BT 474 cells.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid

amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human BT 474 cells. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 5,205.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as

probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 5,205 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 5,206 - 10,317, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 5,205 can be used, or that portion thereof in SEQ ID NOS. 5,206 - 10,317 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

10           Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT<sup>™</sup> Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X<sup>™</sup> Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL<sup>™</sup>) System, New England Biolabs, Beverley, MA)

20           Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

30           It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 5,206 - 10,317. Such amino acid sequences are set out in SEQ ID NOS: 10,318 - 15,438. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, 35 can be conjugated to a carrier protein and used to generate

antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

5

The following examples are offered by way of illustration and not by way of limitation.

#### EXAMPLE 1

#### 10 Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

##### Bioinformatics Results

All human BAC sequences in fewer than 10 pieces  
15 that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the  
20 program CROSS\_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden  
25 Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

30 The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of  
35 genomic sequence called as coding region.



The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence; GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed.

5 That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two  
10 criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb  
15 window.

#### PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification,  
20 as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-  
25 modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per  
30 gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ). A first additional sequence was commonly added to each ORF-unique  
35 5' primer, and a second, different, additional sequence was

commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences  
5 also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the  
10 universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto,  
15 CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band  
20 appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF  
25 length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of  
30  $475 \pm 25$  bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about  
35 500 bp, it was found that long exons had a higher PCR

failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp,  
5 constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and  
10 reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear,  
15 but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with  
20 hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression  
25 ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which  
30 were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average  
35 hybridization signal of which was used as a measure of

background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

5 One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than  $1 \times 10^{-100}$ ) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA  
10 (BLAST E values from  $1 \times 10^{-5}$  to  $1 \times 10^{-99}$ ). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were  
15 then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

20

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase

36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

#### EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1)  
15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in  
20 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia  
25 Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA<sup>+</sup> mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After

snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100 $\mu$ M dATP, 100  $\mu$ M dGTP, 100  $\mu$ M dTTP, 50  $\mu$ M dCTP, 50  $\mu$ M Cy3-dCTP or Cy5-dCTP 50  $\mu$ M, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5.

10 Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30  $\mu$ l hybridization solution

15 containing 50% formamide, 5X SSC, 0.2  $\mu$ g/ $\mu$ l poly(dA), 0.2  $\mu$ g/ $\mu$ l human cot1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

20

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

25

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact,

30 both signal and expression ratios (the latter hereinafter,

35

"expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when  
5 signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is  
10 presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all  
15 tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue  
20 or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class  
25 (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

30 FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative  
35 expression of a clone in that tissue is indicated at the

respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

### Comparison of Signal from Known and Unknown Genes



The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e-30$  (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than  $1e-30$  ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

#### Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic

sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300\_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734\_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed

high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

10 Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normalized Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca <sup>2+</sup> binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a

				synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein

				Phosphatase PP2A, neuronal/ downregulates activated protein kinases
--	--	--	--	---

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be  
 5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca<sup>2+</sup> binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097  
 10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3  
 15 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed  
 20 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless  
 25 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to  
 30 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2

were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often  
 5 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et  
 10 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 $\alpha$  (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics*  
 15 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

20 As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in  
 25 choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a  
 30 commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH
--

	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	$-1.81 \pm 0.11$	$-1.85 \pm 0.08$
Brain	$-1.41 \pm 0.11$	$-1.17 \pm 0.05$
BT474	$1.85 \pm 0.09$	$1.66 \pm 0.12$
Fetal Liver	$-1.62 \pm 0.07$	$-1.41 \pm 0.05$
HBL100	$1.32 \pm 0.05$	$2.64 \pm 0.12$
Heart	$1.16 \pm 0.09$	$1.56 \pm 0.10$
HeLa	$1.11 \pm 0.06$	$1.30 \pm 0.15$
Liver	$-1.62 \pm 0.22$	$-2.07 \pm$
Lung	$-4.95 \pm 0.93$	$-3.75 \pm 0.21$
Placenta	$-3.56 \pm 0.25$	$-3.52 \pm 0.43$

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

### EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the

information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb,



upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):

5 red = kallistatin protease inhibitor (P29622);  
purple = plasma serine protease inhibitor (P05154);  
turquoise =  $\alpha$ 1 anti-chymotrypsin (P01011); mauve = 40S  
ribosomal protein (P08865). Note that chip sequence 8 and  
10 12 did not sequence verify.

#### EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring  
15 Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique  
20 exons in the human genome that could be shown to be expressed at significant levels in BT 474 cells.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon  
25 microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the  
30 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base-incremented fragments of each of the 5,205 single exon probes, each fragment corresponding to an extension product from one of  
35 the two amplification primers.)

The structures of the 5,205 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 5,205. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 5,206 - 10,317, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered

to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean +  
5 (3\*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any  
10 signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human BT 474 cells and thus  
15 presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human BT 474 cells.

The sequence of each of the exon probes identified by SEQ ID NOS.: 5,206 - 10,317 was individually  
20 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were  
25 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted  
30 in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective  
35 probes (by "AMPLICON SEQ ID NO.:" and additionally by the

SEQ ID NO.: of the exon contained within the probe: "EXON  
SEQ ID NO.:" from least similar to sequences known to be  
expressed (i.e., highest BLAST E value), at the beginning  
of the table, to most similar to sequences known to be  
5 expressed (i.e., lowest BLAST E value), at the bottom of  
the table.

Table 4 further provides, for each listed probe,  
the accession number of the database sequence that yielded  
the "Most Similar (top) Hit BLAST E Value", along with the  
10 name of the database in which the database sequence is  
found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.  
corresponding to the predicted amino acid sequences where  
they have been determined for the probe and exon nucleotide  
15 sequences. These are set out as PEPTIDE SEQ ID NOS.: The  
peptide sequences for a given exon are predicted as  
follows: Since each chip exon is a consensus sequence drawn  
from predictions from various exon finding programs (i.e.  
Grail, GeneFinder and GenScan), the multiple initial ORFs  
20 are first determined in a uniform way according to each  
prediction. In particular, the reading frame for predicting  
the first amino acid in the peptide sequence always starts  
with the first base of any codon and ends with the last  
base of non-termination codon. Next, for each strand of the  
25 exon, initial ORFs are merged into one or more final ORFs  
in an exhaustive process based on the following criteria:  
1) the merging ORFs must be overlapping, and 2) the merging  
ORFs must be in the same frame.

The Sequence Listing, which is a superset of all  
30 of the data presented in Table 4, further includes, for  
each probe, the most similar hit, with accession number and  
BLAST E value, from the each of the three queried  
databases.

Table 4 further lists, for each probe, a portion  
35 of the descriptor for the top hit ("Top Hit Descriptor") as

provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about  $1e-05$  and  $1e-100$ ), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of  $1e-05$  (i.e.,  $1 \times 10^{-5}$ ) and  $1e-100$  (i.e.,  $1 \times 10^{-100}$ ) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of  $1e-30$  was used as the boundary when only two classes were to be defined for analysis (unknown,  $>1e-30$ ; known  $<1e-30$ ) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about  $1e-100$  – which is probative evidence that the query sequence has previously been shown to be expressed – the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 – 5,205) and probe exon (SEQ ID NOs.: 5,206 – 10,317, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST

E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

- 5 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

10 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human BT 474 cells

- Table 4 (214 pages) presents expression, homology, and  
15 functional information for the genome-derived single exon probes that are expressed significantly in human BT 474 cells, human epithelial cells isolated from a solid, invasive ductal carcinoma of the breast and available commercially from American Type Culture Collection under  
20 catalogue number HTB-20.

Page 1 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
449	5617	10762	4.28				
880	6040	11211	7.04				
1047	6188		2.6				
1308	6438	11611	12.4				
1627	6755	11949	2.17				
1647	6776	11967	4.24				
1738	6865	12069	1.89				
1761	6887	12093	1.25				
1767	6893	12100	6.38				
1898	7017	12238	0.96				
1980	7097	12328	1.31				
2147	7261	12508	1.73				
2256	7366	12622	2.11				
3167	8318	13480	2.71				
3431	8573	13733	1.47				
3500	8641	13807	11.21				
3547	8688		0.74				
3634	8773	13929	0.93				
3919	9055		0.92				
4169	9295	14433	1.54				
4235	9360	14492	6.08				
4255	9380	14512	0.87				
4256	9380	14513	0.87				
4314	9436		1.18				
4803	9916	15057	1.18				
5026	10128	15257	5.94				
5037	10139	15271	1.46				
2627	7726	12979	2.67	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prMM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2627	7726	12980	2.67	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prMM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2889	8043	13207	2.89	9.4E+00	AB043785.1	NT	Mus musculus A73 gene for antithrombin, complete cds
439	5608	10752	2.06	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
2947	8101	13265	2.56	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds

Page 2 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2947	8101	13266	2.56	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
3510	8651		0.9	5.8E+00	7661557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
4752	9865	15014	1.25	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
4036	9167		10.58	4.8E+00	AF185255.1	NT	Eumecia australis histone H3 (H3) gene, partial cds
287	5476	10617	2.31	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
288	5476	10617	1.99	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3257	8407	13568	1.64	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3012	8166	13323	0.63	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3012	8166	13324	0.63	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3486	8627	13784	5.32	3.8E+00	X64518.1	NT	N. jabacum chitinase gene 50 for class I chitinase C
4298	9420		0.69	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
2595	7696		1.75	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
3694	9128	14272	12.99	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
591	5763	10880	9.75	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
3230	8380	13540	1.12	3.6E+00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
1526	8653	11839	3.27	3.4E+00	AF254377.1	NT	Brassica napus RPB5d mRNA, complete cds
500	5687	10802	1.43	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
3999	5687	10802	0.61	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4696	9812	14960	1.65	3.2E+00	4502404	NT	Homo sapiens carotinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
2799	7956	13121	1.47	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
2008	7126	12362	1.47	2.9E+00	AE002225.2	NT	Chlamydia pneumoniae AR39, section 83 of 94 of the complete genome
1469	6596	11784	7.24	2.8E+00	AF186398.1	NT	Buxus harlandii maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product
1643	6771		1.54	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
229	5423	10560	13.15	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
228	5423	10581	13.15	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
4646	9764	14908	5.56	2.6E+00	AF068749.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
1476	6603	11788	1.77	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1476	6603	11789	1.77	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
2984	8136	13303	0.95	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4881	9992	15139	5.5	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
1257	5386	11563	11.36	2.3E+00	Z46724.1	NT	G. domesticus artificial single chain antibody gene (L3)
4093	9222		1.44	2.3E+00	AJ401081.1	NT	Bos taurus partial cyb gene for cytochrome b
3992	9126	14271	1.39	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds



Page 3 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4290	9412	14547	3.83	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4290	9412	14548	3.83	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
568	7894	10861	6.54	2.1E+00	AF132812.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3676	8716		0.76	2.1E+00	AW449366.1	EST_HUMAN	U1H-B13-ald-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
1189	6332	11501	1.31	2.0E+00	AF180327.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1189	6332	11502	1.31	2.0E+00	AF180327.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1340	6468	11649	0.86	2.0E+00	AF204927.1	NT	Oryctolagus cuniculus Net-K+ATPase beta 1 subunit mRNA, complete cds
1588	6717		2.41	2.0E+00	P25582	SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2133	7247	12492	10.19	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2133	7247	12493	10.19	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4076	9206	14342	1.9	2.0E+00	AW664496.1	EST_HUMAN	h13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
4076	9206	14343	1.9	2.0E+00	AW664496.1	EST_HUMAN	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
3086	8219	13371	1.97	1.8E+00	P21004	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); PROTEIN B8 PRECURSOR
3097	8250	13399	1.92	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3097	8250	13400	1.92	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
1109	6247	11410	2.95	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2250	7360	12617	1.65	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2353	7460	12716	0.98	1.7E+00	AI141067.1	EST_HUMAN	oz43h05.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4438	9557	14699	0.76	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2028	7145	12385	4.48	1.6E+00	AF189339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2037	7155	12394	2.2	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2041	7158	12398	1.13	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2260	7370		1.15	1.6E+00	X98373.1	NT	B.napus gene encoding endo-polygalacturonase
2930	8084	13751	1.56	1.6E+00	W58426.1	EST_HUMAN	zcd25107.1 Soares_fetal_heart_NBH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to
4005	9138		5.78	1.6E+00	BF570077.1	EST_HUMAN	gb:D29805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);
4329	9451	14584	1.52	1.6E+00	AF155827.1	NT	602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4329	9451	14585	1.52	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4329	9451	14585	1.52	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds

Page 4 of 214  
Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5067	10169	15303	2.59	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
6067	10169	15304	2.59	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
31	5242	10358	3.73	1.5E+00	U53449.1	NT	Rattus norvegicus Jun dimerization protein 2 (Jdp-2) mRNA, complete cds
230	5424	10562	2.47	1.5E+00	AE002201.2	NT	Chlamydomonas reinhardtii AR39, section 32 of 94 of the complete genome
618	5778		2.04	1.5E+00	6752861	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2387	7483	12746	1.38	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2486	7590	12839	1.36	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3116	7493	12746	2.41	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3356	8501	13689	0.6	1.6E+00	AE001946.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
28	5239	10354	1.12	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
28	5239	10355	1.12	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2315	7423		5.46	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2630	7728	12984	1.41	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2735	7829	13083	227.51	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2735	7829	13084	227.51	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3315	8462		0.8	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4559	9677		1.67	1.4E+00	BF691547.1	EST_HUMAN	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5031	10133	15283	0.92	1.4E+00	Y19213.1	NT	Homo sapiens putative psitt-bA pseudogene for hair keratin, exons 2 to 7
569	5733		1.6	1.3E+00	Z73640.1	NT	M. musculo gene encoding 4-Dihydroxyethyl-tyrosine dehydrogenase
903	6053	11223	2.56	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 26S rRNA gene, isolate Tibet
1130	6287		23.68	1.3E+00	Y19213.1	NT	Homo sapiens putative psitt-bA pseudogene for hair keratin, exons 2 to 7
1301	6431	11605	12.87	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (ZNF157) mRNA
1301	6431	11606	12.87	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (ZNF157) mRNA
1363	6492		1.49	1.3E+00	U61730.2	NT	Coix lacryma-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
1623	6751		2.09	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2521	7625		1.25	1.3E+00	BE668735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2906	8058	13227	0.74	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythrocyte (Spna1), mRNA
							Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (F55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
3583	8724	13882	0.82	1.3E+00	AF016494.1	NT	
649	5810	10945	8.47	1.2E+00	AA676246.1	EST_HUMAN	2122008.g1 Soares_fetal_liver_spleen_1NF1.S1 Homo sapiens cDNA clone IMAGE:431535 3'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
824	5977	11141	1.11	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
824	5977	11142	1.11	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
824	5977	11143	1.11	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
870	6020		1.11	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1163	6298	11484	6.19	1.2E+00	AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1208	6340	11510	1.88	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1208	6340	11511	1.88	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2356	7463	12718	0.98	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
3086	8239	13388	0.95	1.2E+00	AB020881.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3144	8295	13453	5.63	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3144	8295	13454	5.63	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3270	8419		3.42	1.2E+00	P64910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3336	8482	13648	0.65	1.2E+00	AF168740.1	NT	Homo sapiens LHX3 gene, intron 2
3691	8829	13983	7.07	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3691	8829	13983	7.07	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3691	8829	13983	7.07	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3691	8829	13983	7.07	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4274	8482	13648	1.07	1.2E+00	AF168740.1	NT	Homo sapiens LHX3 gene, intron 2
4450	9569		1.82	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4497	9616	14757	1.04	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4534	9652	14797	1.81	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4582	9880		5.91	1.2E+00	Y09200.1	NT	T. phmatum chloroplast rbcL gene, partial
463	5631	10770	1.04	1.1E+00	D86280.1	NT	Human mRNA for KIAA0227 gene, partial cds
1773	6899	12107	1.22	1.1E+00	AW995393.1	EST_HUMAN	QY0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
3311	8458	13620	5.79	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3311	8458	13621	5.79	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3468	8810	13776	0.7	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3567	8708	13869	0.92	1.1E+00	AI08860.1	EST_HUMAN	wf54h11.x1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2359481 3' similar to
3698	8836	13989	1.48	1.1E+00	AE003395.1	NT	SW:P331_HUMAN Q12888 PES-BINDING PROTEIN 53BP1 ;
3698	8836	13990	1.48	1.1E+00	AE003395.1	NT	Xyella fastidiosa, section 32 of the complete genome
3795	8932		0.73	1.1E+00	X85374.1	NT	Xyella fastidiosa, section 32 of the complete genome
3915	9051	14210	1.01	1.1E+00	8922641	NT	H. parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
3995	9129	14273	0.79	1.1E+00	6755205	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4189	9315		5.62	1.1E+00	5835331	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (PsmB7), mRNA
4655	9772		1.78	1.1E+00	U34992.1	NT	R. unicornis complete mitochondrial genome
4655	9772		1.78	1.1E+00	U34992.1	NT	Carcharias plumbeus Ig lambda light chain gene, complete cds

Page 6 of 214  
Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4978	10086	15221	3.5	1.1E+00	U18468.1	NT	African swine fever virus, complete genome
85	5304		2.28	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
109	5313	10452	1.96	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
417	5585		2.14	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 16S rRNA, 5.8S rRNA and 26S rRNA
574	5738	10865	2.43	1.0E+00	AL251660.1	NT	Giardia lamblia mRNA for homeodomain transcription factor (so gene)
676	5834	10974	8.37	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
677	5835		1.3	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1395	7916		2.27	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
2459	7563	12615	1.02	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2459	7563	12616	1.02	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2841	7998	13154	3.76	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2841	7998	13155	3.76	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2838	8090		0.78	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 97.9 KD PROTEIN C8F12.08C IN CHROMOSOME 1
3182	8333	13498	1.13	1.0E+00	AA628453.1	EST_HUMAN	af26g08.st Soares_total.Jetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3585	5304		0.73	1.0E+00	U23808.1	NT	WP:C42D8.3 CE04204; contains element MER22 MER22 repetitive element;
3658	8787	13953	1.44	1.0E+00	AJ223816.1	NT	Xenopus laevis rhodopsin gene, complete cds
						NT	Agaricus bisporus mRNA for tyrosinase
4044	9175	14316	0.8	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4249	9374		0.68	1.0E+00	8822245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139). mRNA
4773	9886	15032	3.01	1.0E+00	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6134	10234		0.63	1.0E+00	AF200817.1	NT	Pilot whale morbillivirus phosphoprotein (P) gene, partial cds
3590	8730		8.61	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
521	5687	10819	1.56	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYL-GLUTAMATE SYNTHASE)(AGS)(NAGS)
2762	7856		1.19	9.8E-01	AF174644.1	NT	Xenopus laevis rec GTPase mRNA, complete cds
4415	9535	14674	0.66	9.8E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4415	9535	14675	0.66	9.8E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4437	9556	14698	1.62	9.8E-01	AW709674.1	EST_HUMAN	PM2-UM0053-2/0300-005-f12 UM0053 Homo sapiens cDNA
3761	8898	14048	1.92	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3761	8898	14049	1.92	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3184	8335		3.87	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3203	8354		1.98	9.4E-01	AF080595.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds

Page 7 of 214  
Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1745	6871		1.14	9.3E-01	AF242382.1	NT	Homo sapiens phylicoyl-CoA hydroxylase (PHYH) gene, exon 5
2599	7699	12954	2.9	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4009	9142	14282	0.78	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4009	9142	14283	0.78	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
3224	8374	13537	3.14	9.2E-01	BE022702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:39161843
2116	7231		1.21	9.1E-01	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3189	8340	13501	1.03	9.1E-01	T28418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5'
3189	8340	13502	1.03	9.1E-01	T28418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5'
3191	8342	13505	0.78	9.0E-01	7681625	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
4358	9480	14518	1.77	9.0E-01	AF098810.1	NT	Homo sapiens neurixin III-alpha gene, partial cds
5001	10106	15237	0.6	9.0E-01	AF017729.1	NT	Oryctolagus cuniculus Rad51 (RAD51) mRNA, complete cds
4515	8633	14778	1.69	8.8E-01	O28350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
464	5632	10771	1.49	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2380	7486	12740	1.03	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2839	7994	13152	13.39	8.7E-01	AA595863.1	EST_HUMAN	nr05f11.st NCI_CGAP_P14.1 Homo sapiens cDNA clone IMAGE:1076877
							Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
4894	10100		3.43	8.7E-01	AF121970.1	NT	Rat IGF1 gene for insulin-like growth factor II
474	5641		2.14	8.6E-01	X17012.1	NT	zc44ed03.r1 Soares_fetal_heart, NbHH19W Homo sapiens cDNA clone IMAGE:343510 5'
859	6010	11182	6.02	8.6E-01	W69069.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3602	8741	13895	0.66	8.6E-01	AL161565.2	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
3778	8915	14067	1.3	8.6E-01	U49724.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
740	5898	11048	2.34	8.3E-01	M93437.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3068	8221	13372	3.2	8.3E-01	AL161506.2	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
3987	9121	14268	2.82	8.3E-01	Y19177.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2044	7160	12399	1.35	8.2E-01	AB000489.1	NT	Homo sapiens MHC class 1 region
3440	8582	13742	2.55	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
3440	8582	13743	2.55	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
4901	10012		0.83	8.1E-01	AF202834.1	NT	Drosophila melanogaster Na/K-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
172	5367		2.34	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphatase ectyltransferase allele 15
286	5475	10616	12.52	8.0E-01	AJ132772.1	NT	Bos taurus tub and rtf genes
1613	6741	11936	0.96	8.0E-01	8394087	NT	Rattus norvegicus protease (prosome, macropain) 28 subunit, alpha (Psmel), mRNA

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2026	7147		1	8.0E-01	BF530862.1	EST_HUMAN	602072473F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215091 5'
3049	8203	13359	1.08	8.0E-01	AF127897.1	NT	Salimiri boliviensis olfactory receptor (SBO27) gene, partial cds
3294	8441	13603	1.1	8.0E-01	AB006193.1	NT	Mus musculus gene for olfactory glycoprotein, complete cds
3680	8819		1.58	8.0E-01	AL162758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 717
4507	9626	14769	6.59	8.0E-01	X63739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
4966	10074	15212	1.12	8.0E-01	7657352	NT	Mus musculus myosin IXb (Myo9b), mRNA
493	5621	10764	0.97	7.9E-01	D11476.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
713	5870		0.73	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 69 of the complete genome
1618	6746		10.36	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1698	6797		0.99	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2243	7354	12611	4.45	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitaughin29, complete cds
2244	7355	12612	1.07	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3501	8642	13808	2.75	7.9E-01	AF228664.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4277	9400		1.62	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4583	9701	14839	0.91	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4583	9701	14840	0.91	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5140	10240		0.65	7.9E-01	AF139718.1	NT	Chrysomya bezziana peritrophin-48 precursor, gene, complete cds
5158	10258	15397	1.26	7.9E-01	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
877	6027		1.78	7.9E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-14h04
2264	7364	12620	1.48	7.9E-01	AW959567.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4670	9786	14931	1.11	7.9E-01	U87303.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5019	10121		0.75	7.9E-01	AW753353.1	EST_HUMAN	RC3-C10254-130100-023-c02 CT0254 Homo sapiens cDNA
139	5336	10480	4.5	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
724	5880		1.32	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region; major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like
2673	7770	13022	1.32	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE
3337	8483		0.78	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNAc-T7), mRNA
3586	8726	13884	3.69	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4375	9486	14640	3.06	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds

Page 9 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4375	9495	14641	3.06	7.7E-01	AF189488.1	NT	Ootulix columbia japonica sub-species japonica beta-actin mRNA, partial cds
511	5677		1.29	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
582	5745	10873	1.08	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3341	8487	13653	0.96	7.5E-01	C14203.1	EST_HUMAN	C14203 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-037E11 5'
1131	6268	11430	1.4	7.4E-01	AI509146.1	EST_HUMAN	tn14b09.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
2324	7432	12684	0.99	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3707	8845	13999	1.07	7.4E-01	AF112538.1	NT	Maize pusilla actin (Act1) mRNA, complete cds
3878	9014	14171	0.53	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTXphi Calcutta-rsR-a (rsR-a) and Calcutta-rsR-b (rsR-b) genes, complete cds
4288	9410	14546	7.33	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2868	8123	13286	0.83	7.3E-01	P09710	SWISSPROT	HYPOTHEICAL PROTEIN HKLF1 (HKL1) (TRL1)
4587	9705	14843	0.75	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4659	9785	14930	4.1	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
832	5984		1.44	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1961	7078	12302	7.25	7.2E-01	X79140.1	NT	N. tabacum Nelf-4A13 mRNA
3039	8193	13348	1.3	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3434	8576	13736	2.23	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I) allele, complete cds
4735	9848	14894	3.19	7.2E-01	D90314.1	NT	L. mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5098	10198	15336	1.13	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
5098	10198	15337	1.13	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
690	5847	10990	8.62	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3035	8180	13345	12.51	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4180	9306	14442	3.32	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4180	9306	14443	3.32	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
1232	8363	11535	1.64	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1232	6363	11536	1.64	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5038	10140		1.55	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5168	10266	15407	3.95	7.0E-01	T68323.1	EST_HUMAN	yc41h03.s1 Strategene liver (#5377224) Homo sapiens cDNA clone IMAGE:83285 3' similar to gb:K03020 PHENYLALANINE-4-HYDROXYLASE (HUMAN);
971	6118	11287	13.08	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
971	6118	11288	13.08	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1314	6444	11621	1.98	6.9E-01	AA593530.1	EST_HUMAN	nt28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3204	8355	13516	1.41	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
958	6106	11275	1.78	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2635	7733		2.28	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27127, 3418852-3573470
2789	6756	11950	1.22	6.8E-01	AA854476.1	EST_HUMAN	aj75a05.s1 Soares, parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X66411_rna1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4544	9662	14805	1.26	6.8E-01	J00762.1	NT	Rat(hooded) prolactin gene : exon iii and flanks
296	5484	10626	24.41	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
337	5520	10656	16.98	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2131	7245	12489	1.07	6.7E-01	AA451864.1	EST_HUMAN	zx12g12.s1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;
2148	7934	12509	1.89	6.7E-01	AF186073.1	NT	Drosophila melanogaster Msi85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2964	8118	13281	3.1	6.7E-01	6878580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4431	9550	14693	0.64	6.7E-01	X74421.1	NT	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase
4947	10056	15194	1.03	6.7E-01	AW079140.1	EST_HUMAN	xa85g12.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:2574599 3'
2681	7757	13008	1.24	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3470	8612	13778	1.02	6.6E-01	4506880	NT	Homo sapiens serpin domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMASA) mRNA
3635	8774	13630	3.79	6.6E-01	Y07699.1	NT	C. albicans random DNA marker, 282bp
4085	9214		0.72	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5170	10268	15409	1.21	6.6E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68



Page 11 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
622	5762	10912	1.19	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
622	5762	10913	1.19	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3414	8557	13716	4.01	6.5E-01	AB041226.1	NT	Mus musculus gene for Tob2, complete cds
4256	9381	14514	4.73	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5045	10147	15276	2.62	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
248	5440	10580	6.59	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3438	8580	13740	3.26	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3840	8978	14131	1.22	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1807 protein, partial cds
433	5602	10749	3.11	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
533	5999	10831	1.69	6.3E-01	U32699.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2144	7258	12504	1.04	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigenic resistance locus
2642	7846	12895	35.36	6.3E-01	U76331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2542	7845	12896	35.36	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2987	8142		0.7	6.3E-01	Y17275.1	NT	Lycopodium obscurum p89a gene, complete cds
2371	7477		2.11	6.1E-01	6678076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
5192	10289	15426	1.04	6.1E-01	BF314193.1	EST_HUMAN	601901013F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130378 5'
494	5661	10797	1.02	6.0E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
560	5725		2.77	6.0E-01	5802909	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1371	6499	11692	1.83	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH-63-53b attachment protein (G) gene, complete cds
3792	8929	14077	0.82	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4007	9140	14281	1.3	6.0E-01	X16842.1	NT	Xenopus mRNA for desmin
4159	9285		1.94	6.0E-01	AF059895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
1001	6147	11314	2.24	5.9E-01	U92701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
1409	6536	11714	1.11	5.9E-01	6680232	NT	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgcl), mRNA
3253	8403	13594	5.03	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3253	8403	13595	5.03	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4198	9323		5.04	5.9E-01	AF162746.1	NT	Rattus norvegicus cenein 2 mRNA, partial cds
1913	7032	12252	1.08	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
3957	9092	14244	1.09	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4488	9807	14745	4.55	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
4765	9878		0.92	5.8E-01	AF110846.1	NT	Megascalia scalaris sex-lethal homolog (Megsxl) gene, partial cds, alternatively spliced products
1507	6634	11820	0.96	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
1607	6634	11821	0.96	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3015	8169		0.87	5.7E-01	6755253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3208	8359	13520	1.87	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOV01) (MOV01A)
3487	8628		2.46	5.7E-01	AB033503.1	NT	Populus euramericana pease-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
5183	10280	15418	1	5.7E-01	L41867.1	NT	Drosophila extra sex combs gene, exon 1-4, complete cds
3345	8491	13657	1.31	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3345	8491	13658	1.31	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4218	8943	14473	1	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
1214	6346	11516	2.95	5.5E-01	8393912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2662	7758	13009	2.01	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2662	7758	13010	2.01	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2884	8038	13203	0.84	5.5E-01	5902085	NT	Homo sapiens superkiller viralidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3038	8192	13633	1.93	5.5E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2551-B56Y Homo sapiens cDNA clone IMAGE:178266 3'
3219	8370	13633	3.87	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3667	8806	13662	2.13	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
140	5337	10481	12.97	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
140	5337	10482	12.97	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
583	5746	10874	1.14	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
583	5746	10875	1.14	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
1275	6404	11578	2.32	5.4E-01	AW866087.1	EST_HUMAN	QV4-NN0040-070400-180-c04 NN0040 Homo sapiens cDNA
2097	7212	12602	2.04	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 94 of the complete genome
2235	7347	12602	1.13	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
514	5680	10814	2.01	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
2744	7838	13092	12.76	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2744	7838	13093	12.76	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3227	8377	13638	3.1	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSDCL) gene, complete cds

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4184	9310		1.26	5.3E-01	U39687.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
817	5970	11131	9.27	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1166	6301	11467	6.81	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5(T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
1193	6327	11494	3.63	5.2E-01	AF224492.1	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT6)
1894	7013		4.02	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2130	7244	12488	1.46	5.2E-01	AB018283.2	NT	Homo sapiens chromosome 21 segment HS21C085
3096	8249	13398	1.39	5.2E-01	U65942.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3222	8373		0.66	5.2E-01	D73443.1	NT	Chlamydomonas reinhardtii gene for isocitrate dehydrogenase, complete cds
3386	8530		1.73	5.2E-01	AL116780.1	NT	Bacillus cereus strain T4 cDNA library under conditions of nitrogen deprivation
3425	8567	13726	2.15	5.2E-01	AA984165.1	EST_HUMAN	em77g05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3612	8751		1.26	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
4054	8751		0.64	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
5114	10215		1.1	5.2E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
614	5774	10905	2.44	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
647	5808	10942	4.08	5.1E-01	AJ233944.1	NT	Polyglutamine vitellin (strain PI vt1) 16S rRNA gene
647	5808	10943	4.08	5.1E-01	AJ233944.1	NT	Polyglutamine vitellin (strain PI vt1) 16S rRNA gene
1665	6793		1.04	5.1E-01	X87885.1	NT	R. norvegicus mRNA for mammalian fusca protein
4052	9183	14325	4.76	5.1E-01	AI856495.1	EST_HUMAN	wf39b12.x1 NC1 CGAP U11 Homo sapiens cDNA clone IMAGE:2427263 3'
4168	9284	14420	2.66	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
3654	8793	13949	1.16	5.0E-01	AE001785.1	NT	Thermotoga maritima section 97 of 136 of the complete genome
3729	8866	14020	0.77	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3809	8946	14095	1.12	5.0E-01	L38483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3851	8987	14142	3.05	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
790	5944	11104	2.2	4.9E-01	BF571462.1	EST_HUMAN	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1672	6801	11996	1.23	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1911	7030	12250	1.11	4.9E-01	U40669.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
3525	8666		1.14	4.8E-01	AA912842.1	EST_HUMAN	0132403.s1 Scavina_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1625144 3'
3932	9068		1.38	4.7E-01	BE407975.1	EST_HUMAN	601299359F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629198 5'
3724	8862	14015	1.52	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3724	8862	14016	1.52	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5117	10218		1.06	4.6E-01	IM11267.1	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2834	7989	13149	4.74	4.5E-01	AA677086.1	EST_HUMAN	2j55d02.s1 Soares_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3298	8445	13607	4	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3369	8504	13671	1.01	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4001	9134		1.29	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12
4050	9181	14323	1.02	4.5E-01	A1708908.1	EST_HUMAN	COLLAGEN ALPHA 5(V) CHAIN
4147	10317		4.15	4.5E-01	AW873495.1	EST_HUMAN	as96d09.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2353480 3'
4920	10030	15172	1.18	4.5E-01	BE963445.2	EST_HUMAN	ho0g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
2030	7148		2.19	4.4E-01	6980503	NT	601657226R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
2366	7472	12727	2.49	4.4E-01	P49765	SWISSPROT	Mus musculus integral membrane-associated protein 1 (Itgap1), mRNA
3298	8443	13605	1.3	4.4E-01	AF086790.1	NT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3296	8443	13606	1.3	4.4E-01	AF086790.1	NT	Rattus norvegicus SynGAP-5 mRNA, complete cds
3300	8447	13609	2.03	4.4E-01	BF066726.1	EST_HUMAN	Rattus norvegicus SynGAP-5 mRNA, complete cds
4213	8938		1.54	4.4E-01	BE378707.1	EST_HUMAN	7j91d02.y1 NCJ_CGAP_B16 Homo sapiens cDNA clone IMAGE:3393795 5'
410	5578	10726	2.01	4.3E-01	AF155218.1	NT	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
410	5578	10727	2.01	4.3E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
1617	6745	11940	1	4.3E-01	AF155218.1	EST_HUMAN	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
2836	7991		1.96	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
3032	8186	13341	0.81	4.3E-01	AW909477.1	EST_HUMAN	GM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
4123	9251	14388	1.16	4.3E-01	AW935289.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4365	5578	10726	1.2	4.3E-01	AF155218.1	NT	Human somatostatin I gene and flanks
4385	5578	10727	1.2	4.3E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
4936	10046		1.1	4.3E-01	AL161502.2	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
5094	10194		0.99	4.3E-01	8635250	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
1367	7915	11678	1.08	4.2E-01	Q39102	SWISSPROT	Xastia c-nigrum granulovirus, complete genome
3593	8732	13886	4.15	4.2E-01	AE003947.1	NT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3615	8754	13910	0.97	4.2E-01	AI280338.1	EST_HUMAN	Xyella fastidiosa, section 93 of 229 of the complete genome
3690	10316		0.67	4.2E-01	N81203.1	EST_HUMAN	q94b01.x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3857	8993	14150	0.82	4.2E-01	AW835627.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
3955	9090	14243	1.14	4.2E-01	Q04886	SWISSPROT	QVQ-LT0015-180200-127-h01 LT0015 Homo sapiens cDNA
							SOX-3 PROTEIN
4868	9782	14926	5.49	4.2E-01	AA534083.1	EST_HUMAN	nj69d01.s1 NCJ_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS III HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4748	9861	15010	3.83	4.2E-01	R13467.1	EST_HUMAN	Y77E01.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1095	6233	11396	1.45	4.1E-01	A1905481.1	EST_HUMAN	RC-BT091-210189-142 BT091 Homo sapiens cDNA
1104	6242	11405	1.2	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1104	6242	11406	1.2	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2672	7768	13020	1.09	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2806	8059	13228	1.99	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2806	8059	13228	1.99	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
4248	9373	14506	3.92	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoA, isoB, isoC, isoD, isoE and isoF genes
4282	9405	14902	0.72	4.1E-01	AA909267.1	EST_HUMAN	pm33402.s1 Soares_NFL_T_3BC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4637	9755	14902	1.1	4.1E-01	AV747890.1	EST_HUMAN	AV747890 NPC Homo sapiens cDNA clone NPCBDF10 5'
4652	9769	14916	1.23	4.1E-01	AA460067.1	EST_HUMAN	z66d07.r1 Soares_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:798429 5'
1041	6181	11346	0.93	4.0E-01	8404856	NT	Laqueus rubellus mitochondrion, complete genome
1344	6473	11653	1	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1495	6622	10479	2.81	4.0E-01	6679258	NT	Mus musculus platelet-derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2766	5334	10479	2.2	4.0E-01	6678490	NT	Mus musculus ubiquitin-protein ligase e3 component n-recogin (Ubr1), mRNA
2937	8091	13257	1.3	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21G080
2937	8091	13258	1.3	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21G080
3672	8911	13969	2	4.0E-01	AF088903.1	NT	Streptococcus pneumoniae Y1C (Y1C), Y1D (Y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3808	8943	14091	3.15	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3806	8943	14092	3.16	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4786	9999		8.37	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
1387	6515	11897	1.52	3.9E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2805	7704	12960	2.05	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2867	7783	13013	2.86	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2867	7783	13014	2.86	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3070	8223	13374	4.04	3.9E-01	AJ256906.1	NT	Sinorhizobium meliloti epl, syrB2, cys3 genes and orf3
4056	9186	14328	1.34	3.9E-01	BF592611.1	EST_HUMAN	781d01.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
4977	10085	15220	1.65	3.9E-01	BE728697.1	EST_HUMAN	601663948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833699 5'
155	5352		13.75	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
505	5671		9.81	3.8E-01	AB029281.1	NT	Mus musculus pom-1 mRNA for pericentriolar material-1, complete cds
2536	7639	12867	3.74	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myb-like transcription factor (MYB3R-3) mRNA, complete cds
2587	7945	12951	2.31	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
2973	8127		0.91	3.8E-01	AJ251057.1	NT	Human Immunodeficiency virus type 1 complete genome (isolate 98SE-MIP1213)

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3020	8174	13332	1.93	3.8E-01	AF043383.1	NT	Pleuroctes americanus aminopeptidase N (ampN) gene, partial cds
3465	8607	13771	7.75	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3540	8687		0.92	3.8E-01	A1807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3737	8875	14026	0.95	3.8E-01	BE154080.1	EST_HUMAN	PMO-HT0399-200400-010-G01 HT0339 Homo sapiens cDNA
4040	9171	14312	0.75	3.8E-01	AJ271361.2	NT	Takifugu rubripes wnt2 (partial), frank1, cfr and frank2 (partial) genes
5030	10132	15282	1.07	3.8E-01	AF038633.1	NT	Homo sapiens Mpv17 protein (MPV17) gene, partial cds; and urocartin gene, complete cds
2454	7558	12609	4.15	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3442	8584	13745	8.52	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3849	8985	14141	0.7	3.7E-01	AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4207	9332	14485	6.9	3.7E-01	A1218707.1	EST_HUMAN	ck39c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1610188 3'
4297	9419	14552	1.3	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4368	9489	14633	3.08	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 208 of the complete genome
258	5448	10587	0.64	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
906	6142		8.33	3.6E-01	U89241.1	NT	Human mltp gene, partial cds
1318	6447	11626	2.54	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1318	6447	11627	2.54	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1919	7036	12258	3.85	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1919	7038	12259	3.85	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1956	7073	12298	3.26	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2367	7473		1.87	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2864	10314		6.6	3.6E-01	AF109485.1	NT	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
3451	8593	13750	2.12	3.6E-01	X76736.1	NT	H. sapiens cerolotin transporter gene, exons 9 and 10
3451	8593	13757	2.12	3.6E-01	X76736.1	NT	H. sapiens cerolotin transporter gene, exons 9 and 10
4386	9506	14648	1.13	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4686	9802	14948	0.87	3.6E-01	AF071938.1	NT	Mus musculus protein tyrosine kinase Tec (Tec) gene, alternative exons 4 and 4a, exons 5 through 7 and Tec isoform, complete cds
4686	9802	14949	0.97	3.6E-01	AF071938.1	NT	Mus musculus protein tyrosine kinase Tec (Tec) gene, alternative exons 4 and 4a, exons 5 through 7 and Tec isoform, complete cds
4720	9834	14978	0.65	3.6E-01	Y11520.1	NT	Z.mays mRNA for casein kinase II alpha subunit
4761	9874	15026	1.32	3.6E-01	AJ229237.1	NT	Bacteria from anoxic bulk soil 16S rRNA gene (strain XB46)
4997	10103	15234	2.4	3.6E-01	AW339393.1	EST_HUMAN	ha02g04.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2872569 3'
111	5315	10464	0.93	3.5E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
206	5401	10543	2.38	3.5E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
723	5879	11027	1.02	3.5E-01	7703139	NT	Homo sapiens GAP-like protein (LOC51306), mRNA

Page 17 of 214  
Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
723	5879	11028	1.02	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
780	5935	11093	2.99	3.5E-01	BF129796.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1631	6760	11956	1.07	3.5E-01	BF310888.1	EST_HUMAN	601894663F2 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4124244 5'
1651	6779	11971	2.33	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2259	7369	12625	1.03	3.5E-01	P09798	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2571	7944	12626	2.4	3.5E-01	AA223252.1	EST_HUMAN	zr08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
2666	7782		1.11	3.5E-01	U05897.1	NT	Fibrobacter succinogenes S86 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds
3784	8821		1.46	3.5E-01	AA642138.1	EST_HUMAN	nr06003.s1 NCI_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4236	9361	14493	1.91	3.5E-01	AF071263.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
4911	10021	15166	5.47	3.5E-01	M16349.1	NT	Rat leukocyte common antigen (L-Ca) gene, exons 1 through 5
705	5882		1.51	3.4E-01	AJ242656.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
977	6123	11293	5.3	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, colS genes, ori222 and partial inaA gene
1331	6460	11639	2.1	3.4E-01	Y00564.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2379	7485	12739	2	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
2671	8125	13288	0.68	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2671	8125	13289	0.68	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3127	8279	13435	0.98	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3140	8291	13448	6.65	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGB1) mRNA, complete cds
3325	8472	13634	0.7	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3518	8659	13828	5.42	3.4E-01	AF106835.1	NT	Methyovirus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3769	8906		2.04	3.4E-01	BF446010.1	EST_HUMAN	7194e01.x1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
4010	9143		0.92	3.4E-01	AF184614.1	NT	Q9UJ15 DJ18C9.1
4026	9157		1.3	3.4E-01	AA584198.1	EST_HUMAN	Homo sapiens p47-phox (NCF1) gene, complete cds
4613	9731	14868	1.67	3.4E-01	BE086912.1	EST_HUMAN	nc11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4830	10040		4.7	3.4E-01	AJ240973.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
13	5224	10336	7.33	3.3E-01	X07690.1	NT	q195c05.x1 NCI_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1667208 3' similar to contains Alu repetitive element; Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
102	5224	10336	3.15	3.3E-01	X07980.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
447	5815	10761	1.27	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
632	5793	10927	1.14	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1203	6336	11507	5.33	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1311	6441	11618	2.09	3.3E-01	BF568880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1366	6495	11677	1.22	3.3E-01	U43626.1	NT	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster
1619	6747	11941	1.68	3.3E-01	6753685	NT	Mus musculus disintegrin 5 (Digt5), mRNA
1750	6876		2.18	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week 1 Homo sapiens cDNA 5' and
2382	7488		2.55	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (urate phosphate synthetase and orotidine-5-decarboxylase) (UMPS) mRNA
2915	8069	13241	2.39	3.3E-01	AJ251805.1	NT	Bacteriophage phi-Ye03-12 complete genome
2886	8141		0.83	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3027	8181	13337	0.77	3.3E-01	AJ007832.2	NT	Streptomyces argillaceus nithramycin biosynthetic genes
3476	8618	13784	1.15	3.3E-01	AB012822.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3787	8924	14074	1.88	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3796	8933	14080	1.12	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3838	9074	14229	1.56	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3976	9110	14258	1.82	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4346	9468		3.16	3.3E-01	D31682.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4680	9778		1.49	3.3E-01	AF599114.1	EST_HUMAN	tp78512x1 NCI CCAP_U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORT 1 (HUMAN);
4805	8917	15058	1.12	3.3E-01	D64003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766
456	5624		1.78	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
716	5873		0.62	3.2E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1164	6299	11465	11.49	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1286	6415	11591	1.66	3.2E-01	Z60202.1	NT	P. vulgaris arc5-1 gene
1397	6525	11704	5.03	3.2E-01	Q48824	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1784	6910	12118	1.45	3.2E-01	Z36041.1	NT	S.cerevisiae chromosome II reading frame ORF YBR172c
1794	6920	12130	3.15	3.2E-01	AW057194.1	EST_HUMAN	EST369284 MAGC resequences, MAGD Homo sapiens cDNA
1794	6920	12131	3.15	3.2E-01	AW057194.1	EST_HUMAN	EST369284 MAGC resequences, MAGD Homo sapiens cDNA
2142	7256	12502	1.18	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2512	7615		1.29	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxox1), mRNA
3095	8248	13997	0.95	3.2E-01	BF380745.1	EST_HUMAN	IL2-UT0073-180800-181-H11 UT0073 Homo sapiens cDNA
3924	9080		0.65	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4316	9438	14571	1.15	3.2E-01	4759195	NT	Homo sapiens symplekin (SYM) mRNA
4372	9493	14637	1.41	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4476	9596	14735	1.25	3.2E-01	Q10268	SWISSPROT	HYPOTHE TICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4706	9822		7.84	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4248505 5'
4817	9929	15070	1.1	3.2E-01	4557558	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
5188	10285	15421	1.32	3.2E-01	AL161514.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 26
2632	7790	12987	1.36	3.1E-01	R18051.1	EST_HUMAN	ye80h08.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 OM PROTEIN (HUMAN);
2658	7879	13004	2.52	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2658	7879	13005	2.52	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2821	7977		1.06	3.1E-01	AW629036.1	EST_HUMAN	h46h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875391 3'
3153	8304		3.29	3.1E-01	AB028069.1	NT	Mus musculus gene for Ser/Thr kinase KIAMRE, exon 6
3884	9020	14177	1.15	3.1E-01	AJ251588.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4942	10052	15190	0.64	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
71	7859	10418	1.35	3.0E-01	6756083	NT	Mus musculus protein kinase C, epsilon (Pkce), mRNA
251	5442	10582	7.54	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1226	6358	11528	2.11	3.0E-01	AW300400.1	EST_HUMAN	xs83f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1523	6660	11836	3	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
2977	8131		1.03	3.0E-01	AB008677.1	NT	Bos taurus mRNA for UDP-glucuronosyltransferase, complete cds
3186	8339		0.98	3.0E-01	X83615.1	NT	S.pombe p1c1 gene
3186	8347		1.26	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyglutamate lyase, complete cds
3844	8980	14135	1.71	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
3947	9082	14234	0.92	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4487	9606	14744	1.8	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
2229	7341	12594	1.01	2.9E-01	AF222718.1	NT	Chrysodidymus synnotticus mitochondrion, complete genome
3165	8316	13478	1.05	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds
3234	8384	13545	3.56	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3234	8384	13546	3.56	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3873	8009	14165	0.93	2.9E-01	AJ610836.1	EST_HUMAN	tp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4047	9178	14319	0.64	2.9E-01	AB016426.1	NT	Cavia porcellus mRNA for glutathione s-transferase, complete cds
4062	9193		0.65	2.9E-01	AW002902.1	EST_HUMAN	w02f10.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480395 3'
4464	9583	14721	0.94	2.9E-01	AA284468.1	EST_HUMAN	zs57d12.r1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:701691 5' similar to contains Alu repetitive element;
4857	9774		0.73	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5012	10115	15246	5.24	2.9E-01	BF104760.1	EST_HUMAN	601822439F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045616 5'
5012	10115	15247	5.24	2.9E-01	BF104760.1	EST_HUMAN	601822439F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045616 5'
5096	10186		1.02	2.9E-01	AI870899.1	EST_HUMAN	wa06f03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1.12 L1 repetitive element;
5205	10302	16438	0.81	2.9E-01	AV724733.1	EST_HUMAN	AV724733 HTB Homo sapiens cDNA clone HTBFC05 5'
567	5732		3.2	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
572	5735		1.03	2.8E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1084	6223	11390	2.64	2.8E-01	AF166050.1	NT	Guinea guinea oocyte maturation factor Mos (c-mos) gene, partial cds
1281	6410	11585	0.65	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5'
1281	6410	11586	0.65	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5'
1295	6424	11597	0.84	2.8E-01	D88550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1740	6867	12072	2.48	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT0364-120200-065-b05 CT0364 Homo sapiens cDNA
2009	7127	12363	1.22	2.8E-01	AL047620.1	EST_HUMAN	DKFZp686i2321_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp686i2321
2122	7237	12480	0.98	2.8E-01	AW511195.1	EST_HUMAN	hd44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2447	7551	12804	1.43	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2447	7551	12805	1.43	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2518	7622		1.00	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2626	7725	12978	1.16	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2940	8094		1.32	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2941	8095	13261	2.3	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3241	8391	13553	0.73	2.8E-01	4603642	NT	B.taurus microsatellite (ETH121)
3360	8505	13672	0.86	2.8E-01	AF000004.1	NT	Homo sapiens coagulation factor V (proaccelerin, labile factor) (F5) mRNA
3971	9105	14253	1.57	2.8E-01	AE001180.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
4096	9225		0.62	2.8E-01	AE004450.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4170	9296		2.1	2.8E-01	AI050868.1	EST_HUMAN	Pseudomonas aeruginosa PAO1, section 11 of 529 of the complete genome
4434	9553	14696	0.94	2.8E-01	AL02127.2	NT	ov44g10.x1 Soares_Jesús_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
							Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185

Single Exon Probes Expressed in BT474 Cells

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4439	9558	14700	2.82	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4750	9863	15012	0.96	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4750	9863	15013	0.96	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4791	9904	15041	0.9	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4797	9910	15051	2.63	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4830	9942	15084	1.1	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4180129 5'
4855	9967	15112	2.48	2.8E-01	A1272669.1	EST_HUMAN	q159c11.x1 Soares_NhiHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element;
476	5643	10784	2.44	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
610	5770	10899	3.75	2.7E-01	AA450061.1	EST_HUMAN	z639b10.s1 Soares_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1265	6394	11568	2.01	2.7E-01	AB004906.1	NT	Iponboa purpurea transposable element Tip100 gene for transposase, complete cds
1633	6762	12073	1.92	2.7E-01	X79815.1	NT	G.lambiae SR2 gene
1742	6869	12073	2.26	2.7E-01	W58067.1	EST_HUMAN	z622h10.r1 Soares_fetal_heart_Nb1H19W Homo sapiens cDNA clone IMAGE:341443 5'
1788	6912	12120	1.11	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2124	7933	12107	1.06	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular stomatitis virus type 2, promoter region and exon 1
2347	7454	12707	3.72	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITTO088PIU (M88), partial
2432	7636	12789	2.19	2.7E-01	A1310858.1	EST_HUMAN	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
2953	8107	14267	0.77	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060900-385-e03 HT0875 Homo sapiens cDNA
3986	9120	14267	1.94	2.7E-01	A1928015.1	EST_HUMAN	wo92e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
3996	9130	14274	0.68	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
3996	9130	14275	0.68	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4002	9135	14278	2.24	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4865	9977	15123	0.66	2.7E-01	L27516.1	NT	Triticum aestivum (Wcs66) gene, complete cds
5023	10125	10777	3.3	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0288-230200-016-e03 CT0288 Homo sapiens cDNA
489	7891	10777	3.04	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
480	5648	11707	1.08	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cde
1400	6528	11707	1.46	2.6E-01	BE885087.1	EST_HUMAN	801510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1447	6575	11761	1.26	2.6E-01	AB013200.1	NT	Glycine max pseudogene for Bd 30K
1903	7022	12241	4.04	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1903	7022	12242	4.04	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2

Page 22 of 214  
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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							b604d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14889_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2084	7200		4.41	2.6E-01	AW733162.1	EST_HUMAN	B.martinius fbcl gene
2448	7552		2.33	2.6E-01	Y12896.1	NT	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
2517	7621		4.2	2.6E-01	BE272440.1	EST_HUMAN	EST386635 MAGe sequences, MAGM Homo sapiens cDNA
3065	8218		1.12	2.6E-01	AW974531.1	EST_HUMAN	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3568	8709	13870	0.82	2.6E-01	M22342.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3921	8760	13917	2.13	2.6E-01	AF229118.1	NT	EST371360 MAGe sequences, MAGF Homo sapiens cDNA
4076	9206	14341	0.69	2.6E-01	AW959510.1	EST_HUMAN	QY1-BT0630-040-040-132-e03 BT0630 Homo sapiens cDNA
4126	9264	14393	15.62	2.6E-01	BE080598.1	EST_HUMAN	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4334	9456	14593	1.08	2.6E-01	AF175293.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4470	9589	14728	0.67	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4470	9589	14729	0.67	2.6E-01	AB021180.1	NT	ae89d07.r1 Stragene feld rliha 837202 Homo sapiens cDNA clone IMAGE:838477 5'
4621	9639	14786	1.36	2.6E-01	AA457617.1	EST_HUMAN	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*1) mRNA, complete cds
4616	9734	14871	2.91	2.6E-01	U01103.1	NT	Ophrestia radicea maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product y51605.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
4683	9799	14944	1.44	2.6E-01	AF142703.1	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
4956	10064	15203	3.82	2.6E-01	H04658.1	EST_HUMAN	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
238	5431	10570	1.47	2.5E-01	4502296	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
239	5431	10570	1.65	2.5E-01	4502296	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
252	5443		4.63	2.5E-01	M26501.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
833	5985	11152	1.13	2.5E-01	U09964.1	NT	y511g07.r1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:117468 5'
1061	6202		0.83	2.5E-01	AE002156.1	NT	Olea europaea OEW mRNA for lipoel synthase, complete cds
1122	6260	11425	10.45	2.5E-01	T89837.1	EST_HUMAN	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1388	6516		0.98	2.5E-01	AB025343.1	NT	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
1741	6868		3.12	2.5E-01	4885406	NT	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
1891	7929	12230	1.19	2.5E-01	BE686604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
1891	7929	12231	1.19	2.5E-01	BE686604.1	EST_HUMAN	

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2384	7490		2.19	2.5E-01	AE000875.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2467	7571		1.12	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:694862 5'
3394	8538		3.28	2.5E-01	AW973471.1	EST_HUMAN	EST385464 MAGE resequences, MAGM Homo sapiens cDNA
3522	8663	13830	1.17	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3536	8678	13839	6.55	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3824	8960	14108	1.49	2.5E-01	AJ741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3824	8960	14109	1.49	2.5E-01	AJ741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4043	9174		0.84	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4295	9417		0.79	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4714	9830		1.19	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4721	9835	14979	3.61	2.5E-01	AF007768.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4749	9862	15011	1.98	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4771	9884		3.4	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5'LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
5203	10300	15437	24.99	2.5E-01	U57838.1	NT	Arabidopsis thaliana FK506 binding protein FKBP62 (ROF1) gene, complete cds
552	5717	10849	0.74	2.4E-01	AA936316.1	EST_HUMAN	on70d04.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
849	6000	11172	2.06	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1308	6438	11613	13.62	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1308	6438	11614	13.62	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1394	5522	11701	1.03	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1862	5982		7.18	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1906	7025	12445	0.08	2.4E-01	AF251708.1	NT	Zaocys dhumnades fucose-1,6-bisphosphatase mRNA, complete cds
2242	7353	12610	1.8	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2510	7613	12863	1.72	2.4E-01	Z36534.1	NT	D. discoideum (Ax3-K) ponA gene
2723	7818	13074	1.33	2.4E-01	X71783.1	NT	S. pombe swf6 gene
2747	7841	13088	3.47	2.4E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
3110	8263		2.59	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3126	8278	13434	1.77	2.4E-01	X74209.1	NT	H. sapiens AGT gene, full fragment of intron 4
3741	8879	14030	0.82	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4004	9137		0.68	2.4E-01	D29960.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
4882	9893	15140	9.08	2.4E-01	BE160080.1	EST_HUMAN	QV1-H10412-020400-136-b10 HT0412 Homo sapiens cDNA
387	5556	10700	0.87	2.3E-01	S75898.1	NT	aromatase [Poephila guttata-zebra finches, ovary, mRNA, 3189 nt]
636	5797		5.1	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome

Page 24 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
666	6826	10964	17.78	2.3E-01	U67986.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
935	8083	11248	3.03	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1524	6651	11837	1.01	2.3E-01	6677980	NT	Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA
1642	6770	11964	2.22	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
2039	7156		1.14	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2423	7528	12780	1.37	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2612	7711	12964	1.05	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2784	6823	11702	2.19	2.3E-01	AB015033.1	NT	Marrilabilia agarivorans gyb gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
2932	8086	13253	0.87	2.3E-01	AA601379.1	EST_HUMAN	no16d06.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THR repetitive element;
3056	8209		5.29	2.3E-01	R21732.1	EST_HUMAN	yh21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3352	8497	13666	0.8	2.3E-01	H69836.1	EST_HUMAN	yg97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3489	8630	13787	0.84	2.3E-01	4502054	NT	Homo sapiens atachidionate 15-lipoxygenase (ALOX15) mRNA
3818	8955	14103	1.02	2.3E-01	S82821.1	NT	GSTA5-glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3908	9044		5.06	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4327	9449	14582	0.7	2.3E-01	R82252.1	EST_HUMAN	Y17101.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4379	9500		1.33	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4429	9548	14690	0.7	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4465	9584	14722	2.1	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4527	9845	14792	6.45	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5053	10155	15286	0.91	2.3E-01	BF316135.1	EST_HUMAN	601896136F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125368 5'
5171	10269	15410	1.05	2.3E-01	AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5195	10292	15429	0.65	2.3E-01	U45324.1	NT	Human Kruppel-related 3 (HKR3) gene, exons 1-3
85	5294	10434	0.72	2.2E-01	AI052190.1	EST_HUMAN	oz14a10.x1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to
1680	6709	11900	2.93	2.2E-01	AF187850.1	NT	TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
2014	7131		2.57	2.2E-01	AF171901.1	NT	Homo sapiens PPAR delta gene, promoter region
2082	7198	12443	1.53	2.2E-01	M34640.1	NT	Trimeresurus malabaricus cytb gene, partial cds; mitochondrial gene for mitochondrial product
2381	7487	12741	2.76	2.2E-01	BF077538.1	EST_HUMAN	Fresh-water sponge Emr1 alpha collagen (COLF1) gene
2549	7652	12901	1.39	2.2E-01	BE618258.1	EST_HUMAN	602085608F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:4249669 5'
2548	7652	12902	1.39	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2646	8003	13163	4.77	2.2E-01	BE155925.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2848	8003	13164	4.77	2.2E-01	BE155925.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
							PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA

Page 25 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2886	8040		1.5	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphatase (FHT) gene, exon 5
3373	8518		2.23	2.2E-01	AL161582.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3791	8928		1.47	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4185	9311		0.92	2.2E-01	AF19102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4195	9320	14452	5.31	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4237	9362	14494	2.75	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4237	9362	14495	2.75	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4333	9455	14591	1.02	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4333	9455	14592	1.02	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4477	9597	14736	0.95	2.2E-01	Z54148.1	NT	B. abortus bp28 gene
4794	9907		1.27	2.2E-01	D30604.1	NT	Human beta-cytoplasmic actin (ACTBP5) pseudogene
4799	9912	15053	3.51	2.2E-01	AA211216.1	EST_HUMAN	z987c05.r1 Striatagene NNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648868 5'
5025	10127		1.41	2.2E-01	L13299.1	NT	Mus musculus Vinculin gene, exon 3
5099	10199	15338	1.08	2.2E-01	BE141038.1	EST_HUMAN	MRO-HT0087-201099-002-c10 HT0087 Homo sapiens cDNA
5115	10216		0.95	2.2E-01	S57585.1	NT	histamine H2-receptor [rats, Genomic, 1928 nt]
5145	10245	15383	1.83	2.2E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
5194	10291	15428	0.96	2.2E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
5200	10297	15434	1.8	2.2E-01	H60548.1	EST_HUMAN	y42h00.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208001 5' similar to gb:Z14118.na1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
972	6119	11289	1.38	2.1E-01	AA569289.1	EST_HUMAN	nm31e11.s1 NC1 CGAP Lip2 Homo sapiens cDNA clone IMAGE:1061804
975	6121	11291	0.97	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1125	6202		2.16	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1201	6334	11503	1.11	2.1E-01	6754298	NT	Mus musculus interferon (alpha and beta) receptor 2 (Inar2), mRNA
1201	6334	11504	1.11	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Inar2), mRNA
1916	7035	12255	1.16	2.1E-01	AA908824.1	EST_HUMAN	ek73e02.s1 NC1 CGAP GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765
2139	7253	12499	1.88	2.1E-01	BF69073.1	EST_HUMAN	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247603 5'
2890	8044	13208	1.93	2.1E-01	5912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3785	8922		6.31	2.1E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
4028	9169	14302	1.27	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit-Accession No.	Top Hit Database Source	Top Hit Descriptor
4028	9159	14303	1.27	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4356	9477		1.69	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4549	9867	14800	2.37	2.1E-01	AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
5056	10156	15209	1.15	2.1E-01	Q01338	SWISSPROT	ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)
5156	10256		0.68	2.1E-01	AF135027.1	NT	Homo sapiens sialic acid-binding immunoglobulin-like lectin-9 (SIGLEC9) gene, complete cds
197	5392	10536	1.91	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avena, complete cds
532	5698		2.13	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
697	5854	10909	1.44	2.0E-01	M77085.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allotype V-Ha2
811	5964	11126	1.59	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
1012	6155	11321	0.63	2.0E-01	D90805.1	NT	Synechocystis sp. PCC6803 complete genome, 7127, 781449-920915
1126	6263	11427	2.67	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1258	6387	11564	1.19	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1312	6442	11610	1.56	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291289-002-c06 HT0422 Homo sapiens cDNA
1471	6598		1.61	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1497	6624	11812	2.99	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1567	6695	11882	4.68	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1572	6700	11888	1.65	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1710	6838	12039	1.27	2.0E-01	U23246.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1732	6859		1.48	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1769	6895		2.1	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 87 of 150 of the complete genome
1897	7016	12236	1.08	2.0E-01	BE871330.1	EST_HUMAN	601416441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:38553330 5'
1897	7016	12237	1.08	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:38553330 5'
2327	7435		1.03	2.0E-01	X82877.1	NT	H. sapiens Na+-D-glucose cotransport regulator gene
							xpT5502.x1 NCI CGAP_HIN8 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3555	8696		0.84	2.0E-01	AW238005.1	EST_HUMAN	MER21 repetitive element;
3684	8823	13979	0.64	2.0E-01	P34641	SWISSPROT	GED-11 PROTEIN
3689	8828		0.71	2.0E-01	6680797	NT	Mus musculus bone morphogenetic protein 6 (Bmp6), mRNA
3927	9063	14221	0.83	2.0E-01	Z46906.1	NT	Sua serofa
4003	9136	14279	0.78	2.0E-01	X83997.1	NT	C.parasitica eapC gene
4409	9529	14669	0.74	2.0E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exon 2-9 and 11-16
4538	9556		7.82	2.0E-01	BE826165.1	EST_HUMAN	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
5022	10124	15256	5.58	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5087	10187	15326	0.98	2.0E-01	Y19216.1	NT	Homo sapiens putative palHbD pseudogene for hair keratin, exons 1 to 9



Page 27 of 214  
Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5169	10267	15408	48.35	2.0E-01	Y14980.1	NT	Acinetobacter baumannii fur gene
106	5310		7.75	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
348	5532	10671	4.99	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
655	5816	10963	1.43	1.9E-01	U32581.2	NT	Homo sapiens lambda/ida protein kinase C-interacting protein mRNA, complete cds
655	5816	10954	1.43	1.9E-01	U32581.2	NT	Homo sapiens lambda/ida protein kinase C-interacting protein mRNA, complete cds
662	5823	10981	5.59	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
663	5823	10981	4.32	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
987	6133		1.34	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (IL2rg), mRNA
1105	6243	11407	7.57	1.9E-01	AA358813.1	EST_HUMAN	EST67784 Fetal Lung II Homo sapiens cDNA 5' end
1379	6507	11688	1.76	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1445	6573		2.28	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2361	7488	12723	1.77	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2888	8042	13206	4.43	1.9E-01	U63066.1	NT	Sigmodon hispidus p53 gene, partial cds
2904	8057		5.64	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
2972	8126	13290	0.97	1.9E-01	U25148.1	NT	Rattus norvegicus brush border myosin-I (BBMI) mRNA, partial cds
3376	8521	13685	3.57	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3461	8603	13767	4.34	1.9E-01	R16467.1	EST_HUMAN	YF42F10.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:129547 5'
3783	8920	14071	0.77	1.9E-01	AF284017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
3967	9102	14250	4.13	1.9E-01	AB006784.1	NT	Schistosoma mansoni DNA for cytoplasmic dynein heavy chain, complete cds
4060	9191	14332	1.39	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4209	9334	14460	1.02	1.9E-01	BE634943.1	EST_HUMAN	MR1-FN0010-290700-007-004 FN0010 Homo sapiens cDNA
4448	9567	14708	0.99	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
4998	10104		0.98	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
30	5241	10357	2.94	1.8E-01	U73200.1	NT	Mus musculus Cclg gene for chaperonin containing TCP-1 gamma subunit, partial cds
257	7887	10586	1.87	1.8E-01	AB022090.1	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
368	5548	10692	1.14	1.8E-01	4502632	NT	Oryza latipes gene for membrane guanylate cyclase OIGC1, complete cds
745	5801	11055	0.7	1.8E-01	AB021490.2	NT	wd71602.1 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
983	8129	11297	0.65	1.8E-01	AJ912212.1	EST_HUMAN	Dichostelium discoideum plasmid Ddp5, complete genome
1092	6230	11394	1.22	1.8E-01	AF000580.1	NT	Yersinia pestis plasmid pCD1
1292	6421	11596	5.95	1.8E-01	AL117180.1	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1518	6845	11631	1.83	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1518	6645	11832	1.83	1.8E-01	6753947	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1858	5978		1.09	1.8E-01	4503036	NT	

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1877	6997		1.21	1.8E-01	AI733708.1	EST_HUMAN	qg22d10.x5 NCI_CGAP_KiB3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O756936 O756936 GAMMA BUTYROBETAINE HYDROXYLASE ;
1918	7037	12257	1.29	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A6 precursor, complete cds
2653	7751		1.44	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-038-g04 DT0018 Homo sapiens cDNA
2863	8018		1.78	1.8E-01	AF184589.1	NT	Jonopsidium acaule LEAFY protein (LEAFY2) gene, partial cds
2868	8022	13189	1.54	1.8E-01	AW182300.1	EST_HUMAN	x41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3101	8254	13404	2.1	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3348	8493	13660	0.63	1.8E-01	BF193582.1	EST_HUMAN	G01808723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'
3604	8743	13897	0.78	1.8E-01	H03369.1	EST_HUMAN	Y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
3604	8743	13898	0.78	1.8E-01	H03369.1	EST_HUMAN	Y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
4309	9431		0.89	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BcLA-DQB), complete cds
4529	9647	14793	5.61	1.8E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4736	9851	14998	2.65	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4774	9887	15033	1.05	1.8E-01	X92179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
4837	9949	15093	50.8	1.8E-01	AA383750.1	EST_HUMAN	EST97196 Testis 1 Homo sapiens cDNA 5' end
5027	10126	15258	1.83	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-g06 ST0203 Homo sapiens cDNA
5041	10143	15273	0.96	1.8E-01	AI792382.1	EST_HUMAN	an28g07.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5079	10180	15316	10.32	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5092	10192	15332	0.91	1.8E-01	AI439881.1	EST_HUMAN	t157e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5133	10233	15369	11.74	1.8E-01	AJ132844.1	NT	Broad bean wilt virus 2 genes encoding 118kDa protein, 104kDa protein, large coat protein, small coat protein
5133	10233	15370	11.74	1.8E-01	AJ132844.1	NT	Broad bean wilt virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein
575	5739	10666	1.63	1.7E-01	BE385164.1	EST_HUMAN	G01274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
808	5959	11122	2.09	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
962	5110		1.5	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1983	7100		1.85	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product

Page 29 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2823	7979	13138	2.4	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2823	7979	13139	2.4	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2892	8046	13211	1.36	1.7E-01	AA338809.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2965	8119	13282	1.14	1.7E-01	AJ238736.1	NT	Naja naja atra ctk-1 gene, exons 1-3
2966	8119	13283	1.14	1.7E-01	AJ238736.1	NT	Naja naja atra ctk-1 gene, exons 1-3
3081	8234	13384	1.61	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3347	8492	13659	0.61	1.7E-01	N65763.1	EST_HUMAN	J2346f Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3428	8570	13730	1.32	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3911	9047	14206	5.39	1.7E-01	AJ238377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial Intron 10 of the ALL-1/MLL-HRX gene fused to intron 5 of the AF-4/FEL gene
4533	9651		1.76	1.7E-01	X52936.1	NT	Schistosoma gregaria alpha repetitive DNA
4806	9918	15059	1.16	1.7E-01	AI247635.1	EST_HUMAN	qh57e09.x1 Soares_fetal_liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element
5103	10204		1.17	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (ae) gene, complete cds
5138	10298	15374	0.62	1.7E-01	BF030010.1	EST_HUMAN	601557256F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
121	5321	10465	1.23	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
678	7865	10976	1.15	1.6E-01	R31497.1	EST_HUMAN	yh75f12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1519	6646	11833	1.19	1.6E-01	AA548963.1	EST_HUMAN	nk28d12.61 NCJ_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014839 3'
1637	6684	11850	3.14	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1929	7048	12269	1.14	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2363	7939	12726	1.35	1.6E-01	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2385	7491	12744	1.94	1.6E-01	AL161533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
2858	8013	13176	33.76	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2858	8013	13177	33.76	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3613	8752	13908	1.03	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3613	8752	13909	1.03	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3975	9109		2.81	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4305	9427	14562	10.51	1.6E-01	AF179580.1	NT	Homo sapiens apelin gene, complete cds
4435	9554		2.91	1.6E-01	AW988601.1	EST_HUMAN	EST380877 IMAGE resequences, MAGJ Homo sapiens cDNA

Page 30 of 214  
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Single Exon Probes Expressed in BT474 Cells

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4443	9562		4.45	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4922	10032	15173	1.22	1.6E-01	AA088343.1	EST_HUMAN	z184h08.c1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E2218955
4962	10060	15108	1.54	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV ;
4952	10060	15189	1.54	1.6E-01	AJ006356.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
5101	10201	15339	1.02	1.6E-01	AL353984.1	EST_HUMAN	Lycopodium obscurum RsaI fragment 2, satellite region
5101	10201	15340	1.02	1.6E-01	AL353984.1	EST_HUMAN	DKFZp434O1729_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434O1729 5'
5186	10283	15420	0.97	1.6E-01	AL161884.2	NT	DKFZp434O1729_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434O1729 5'
245	5436	10575	1.59	1.5E-01	BE710087.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
245	5436	10578	1.59	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
585	7864		2.03	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
783	9338	11096	1.83	1.5E-01	AL193284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1093	6231	11395	0.84	1.5E-01	AJ009735.1	NT	Gyrinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1098	6236	11399	2.29	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLG22A2 gene for organic cation transporter (OCT2), exon 1
1114	6252		1.53	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1219	6351	11520	1.03	1.5E-01	AW195616.1	EST_HUMAN	xn39d11.x1 NCL CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2596085 3'
1279	8408	11582	3.97	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1279	8408	11583	3.97	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1492	6619	11809	1.96	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
2879	8033		1.16	1.5E-01	AW572516.1	EST_HUMAN	xx56a02.x2 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X55072_mai
3007	8161	13318	0.89	1.5E-01	MB1441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3334	8480	13646	4.16	1.5E-01	AA935049.1	EST_HUMAN	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3350	8495	13663	0.81	1.5E-01	Z23104.1	EST_HUMAN	cc68d05.x1 NCL CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3350	8495	13664	0.81	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
3736	8874	14025	2.53	1.5E-01	U06964.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3752	8889	14040	1.34	1.5E-01	7108358	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3846	8982	14137	2.23	1.5E-01	AW565983.1	EST_HUMAN	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
4024	9166	14300	0.99	1.5E-01	AW366859.1	EST_HUMAN	h110106.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
4154	9280	14416	8.53	1.5E-01	AL193284.2	NT	RC2-HT0149-191099-012-009 HT0149 Homo sapiens cDNA
4693	9809	14956	1.55	1.5E-01	BF697665.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084

Page 31 of 214  
Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4716	7769	13021	2.25	1.5E-01	BF695381.1	EST_HUMAN	602083209F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4758	9871	15021	1.16	1.6E-01	BE173796.1	EST_HUMAN	GM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4758	9871	15022	1.16	1.5E-01	BE173796.1	EST_HUMAN	GM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4985	10093	15224	1.21	1.5E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
287	5486		0.88	1.4E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV85AP to TCRBV21S2A2 region
911	6081		2.65	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1263	6392		2.4	1.4E-01	T91864.1	EST_HUMAN	Yd54c01.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:112032 3'
1760	6866		1.38	1.4E-01	6678980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1763	6869	12095	1.83	1.4E-01	AE001710.1	NT	Thermoboga maritima section 22 of 136 of the complete genome
1986	7103		8.62	1.4E-01	AA720615.1	EST_HUMAN	ny72407.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2753	7847	13103	2.03	1.4E-01	AI933496.1	EST_HUMAN	wm74d01.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
3875	9011	14107	1	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
3875	9011	14108	1	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
4145	9273	14410	8.95	1.4E-01	AI699094.1	EST_HUMAN	tx56c02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4145	9273	14411	8.95	1.4E-01	AI699094.1	EST_HUMAN	tx56c02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4215	9340	14472	3.21	1.4E-01	AE001710.1	NT	Thermoboga maritima section 22 of 136 of the complete genome
4648	9786	14911	0.76	1.4E-01	5453861	NT	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA
320	5508	10644	1.71	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
320	5508	10645	1.71	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
527	5693	10825	2.26	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
635	5798	10930	0.94	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
635	5798	10931	0.94	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
845	5986	11167	0.82	1.3E-01	X63330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
895	6045	11216	1.34	1.3E-01	AF139918.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1028	6189	11334	1.59	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1128	6295		2.22	1.3E-01	AL115265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1218	6350	11519	2.48	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'
1455	6682		0.96	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein GMS mRNA, complete cds
1963	7080	12304	1.49	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2287	7377		1.09	1.3E-01	AW612104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2360	7467		1.82	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2548	7651	12800	1.78	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3338	8484	13650	1.12	1.3E-01	AF196779.1	NT	Homo sapiens transcription factor GCHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha$ -
3432	8574	13734	0.9	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolyl transacylase mRNA, complete cds
3702	8840	13994	1.39	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (177)
3702	8840	13995	1.39	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (177)
3709	8847	14001	0.7	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrodipicol dehydrogenase 4 [AKR 1C4], exon 2
3781	8918	14069	0.87	1.3E-01	6978940	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
3863	8098		1.48	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4025	5796	10930	0.77	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/JUK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/JUK
4025	5786	10931	0.77	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/JUK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/JUK
4109	9237		1.01	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4130	9258		3.02	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081299-038-a03 DT0018 Homo sapiens cDNA
4137	9265	14404	1.97	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4157	9283	14419	17.16	1.3E-01	AW273741.1	EST_HUMAN	XV23F10.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4284	9389	14526	1.08	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPJ Homo sapiens cDNA clone NPDAZE02 5'
4284	9389	14527	1.08	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPJ Homo sapiens cDNA clone NPDAZE02 5'
4291	9413		1.43	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4458	9577	14715	0.69	1.3E-01	M21672.1	NT	Bovine branched chain alpha-keto acid dihydrolyl transacylase mRNA, complete cds
4508	9627	14770	2.33	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
4915	10025		0.97	1.3E-01	Y12664.1	NT	H. sapiens gene encoding translin, exon 3
381	6690	10735	12.86	1.2E-01	AA421744.1	EST_HUMAN	tt39002.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_mai
423	5210		1.77	1.2E-01	U66912.1	NT	ANNEXIN V (HUMAN);
546	5711		2.49	1.2E-01	AF039442.1	NT	Dictyostellium discoideum ORF DG1016 gene, partial cds
1366	6914	11695	2.43	1.2E-01	AF149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1386	6914	11696	2.43	1.2E-01	AF149146.1	EST_HUMAN	AL149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1393	6621		2.74	1.2E-01	AV735249.1	EST_HUMAN	AL149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1522	6649		1.04	1.2E-01	AA897474.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdAAJB11 5'
							al48e09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480584 3' similar to TR:Q16671
							Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR.;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1641	6769	11983	1.4	1.2E-01	Q14934	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1663	6791	11987	2.95	1.2E-01	A1265402.1	EST_HUMAN	q169f09.x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1960553 3'
1770	6905		6.41	1.2E-01	X99211.1	NT	H.sapiens DNA for endogenous retroviral like element
1923	7042		3.35	1.2E-01	AW449368.1	EST_HUMAN	U1-H-B13-akt-e-10-0-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2164	7277	12524	1.94	1.2E-01	BF248490.1	EST_HUMAN	601821677F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2551	7654	12904	2.18	1.2E-01	AW998556.1	EST_HUMAN	QY3-BN0046-220300-129-110 BN0046 Homo sapiens cDNA
2557	7659	12912	16.53	1.2E-01	BE219889.1	EST_HUMAN	h65504.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178303 3'
2805	7961	13124	1.38	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2867	8021	13188	2.04	1.2E-01	A1720470.1	EST_HUMAN	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:U05095
2900	8054	13223	3.27	1.2E-01	M16364.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
2976	8130	13294	0.74	1.2E-01	X56882.1	NT	Human creatine kinase-B mRNA, complete cds
3215	8366	13330	1.77	1.2E-01	AW370688.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3240	8390		0.72	1.2E-01	U67600.1	NT	QY1-BT0259-261099-021-405 BT0259 Homo sapiens cDNA
3460	8602		0.61	1.2E-01	Z99118.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3507	8648	13814	1.25	1.2E-01	X56882.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3507	8648	13815	1.25	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3591	8802		0.84	1.2E-01	Z99118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3750	8887		0.78	1.2E-01	BF128551.1	EST_HUMAN	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
4163	9276	14414	1.91	1.2E-01	Z54255.1	NT	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053668 3'
4163	9279	14415	1.91	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
4739	9852		2.5	1.2E-01	L32873.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
5029	10131	15260	1	1.2E-01	BE173168.1	EST_HUMAN	Arabidopsis thaliana homeodomain protein (GLABRA2) gene, complete cds
5029	10131	15261	1	1.2E-01	BE173168.1	EST_HUMAN	MRO-HT0559-240-00-016-c09 HT0559 Homo sapiens cDNA
5063	10165		1.01	1.2E-01	P16498	SWISSPROT	MRO-HT0559-240-00-016-c09 HT0559 Homo sapiens cDNA
563	5728	10858	0.7	1.1E-01	A1561003.1	EST_HUMAN	HEMOLYSIN PRECURSOR
612	5772	10902	2.13	1.1E-01	AA569006.1	EST_HUMAN	h18408.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2187983 3'
1056	6197	11362	1.37	1.1E-01	BF697308.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Cc10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_rna1
1086	6225		1.4	1.1E-01	AL161560.2	NT	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1161	7910	11462	3.53	1.1E-01	AW972168.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1253	6383	11561	1.31	1.1E-01	D64004.1	NT	EST384142 IMAGE resequences, MAGL Homo sapiens cDNA
1535	6602	11848	2.07	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2868787-3002965

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2292	7401		1.57	1.1E-01	6756216	NT	Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA
2818	7974	13133	1.1	1.1E-01	S82418.1	NT	interleukin-12 p35 subunit [mice, Genomic, 700 nt, segment 4 of 5]
3005	8159	13316	0.89	1.1E-01	F03265.1	EST_HUMAN	HSC1Rf022 normalized infant brain cDNA Homo sapiens cDNA clone c-1r02 3'
3323	8470		1.44	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3402	8546	13705	2.31	1.1E-01	BE363186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3827066 5'
3433	8575	13735	1.36	1.1E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3472	8614	13781	0.63	1.1E-01	R96946.1	EST_HUMAN	y62g08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains
3570	8711	13871	0.78	1.1E-01	Y07695.1	NT	Alu repetitive element
3687	8828	13981	1.31	1.1E-01	X52708.1	NT	A.immerus gene for transposase
4086	9215	14348	0.85	1.1E-01	AW819412.1	EST_HUMAN	G.gallus gene encoding non-histone chromosomal protein HM1G-14b, exons 4 and 5
4229	9354	14349	0.85	1.1E-01	AW819412.1	EST_HUMAN	MR3-S10290-290100-025-g07 S10290 Homo sapiens cDNA
4261	9386	14523	7.73	1.1E-01	AF157066.1	NT	Drosophila melanogaster kdsrcht protein (klar) mRNA, complete cds
4800	9913	15054	0.65	1.1E-01	AW802056.1	EST_HUMAN	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
			1.32	1.1E-01	Y07695.1	NT	A.immerus gene for transposase
5006	9219		0.6	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
1204	9337		3.9	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1276	6405	11579	2.88	1.0E-01	A1985499.1	EST_HUMAN	ws08d01.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13
1399	6527	11706	1.81	1.0E-01	AL161604.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3498	8639	13805	1.03	1.0E-01	BF033991.1	EST_HUMAN	601456307F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859849 5'
3699	8837	13991	0.92	1.0E-01	BF239818.1	EST_HUMAN	601908489F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4134071 5'
3813	8950	14097	0.98	1.0E-01	AF297061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3813	8950	14098	0.98	1.0E-01	AF297061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3826	8062	14220	2.33	1.0E-01	BF365703.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4528	8946		0.81	1.0E-01	A1792349.1	EST_HUMAN	an32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4880	9786	14941	1.02	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (ter) mRNA, complete cds
4903	10013	15157	2.26	1.0E-01	AW952344.1	EST_HUMAN	EST1364414 MAGE resequences, MAGEB Homo sapiens cDNA
5108	10207	15344	1.08	1.0E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
2739	7833	13086	0.95	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-Ril) mRNA, complete cds
2748	7842	13097	1.36	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'



Page 35 of 214  
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2748	7842	13098	1.36	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456385 5'
3249	8398	13560	1.23	9.9E-02	AF0909810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
592	5727		1.69	9.6E-02	X56338.1	NT	O. sativa RAm3C gene for alpha-amylase
3078	8231		1.57	9.8E-02	4504578	NT	Homo sapiens I factor (complement) (IF) mRNA
3123	8275	13430	3.74	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4201	9326	14457	6.41	9.8E-02	AF257329.1	NT	Leposphaeria maculans beta-tubulin mRNA, complete cds
4201	9326	14458	6.41	9.8E-02	AF257329.1	NT	Leposphaeria maculans beta-tubulin mRNA, complete cds
1357	6486	11667	1.12	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
2241	7352	12609	1.36	9.7E-02	BE168680.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
3956	9091		3.81	9.7E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
4322	9444	14577	3.44	9.6E-02	Z32688.2	NT	Proteus mirabilis fibrinolysin operon, strain HI4320
4957	10094	16226	1.27	9.6E-02	AW068230.1	EST_HUMAN	EST1376303 MAGE resequences, MAGI Homo sapiens cDNA
4077	9207	14344	1.88	9.5E-02	AW992395.1	EST_HUMAN	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
1847	6988	12188	2.28	9.4E-02	BF071063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
3858	8994	14151	5.14	9.4E-02	Z33059.1	NT	M. capricolus DNA for CONTIG MC073
2958	8112		1.78	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3000	8155		6.59	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3238	8369	13552	1.84	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4124	9252	14389	3.24	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4124	9252	14390	3.24	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4703	9816		1.91	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA08 5'
227	5421	10556	7.03	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
227	5421	10557	7.03	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
227	5421	10558	7.03	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2209	7321		6.16	9.2E-02	R54156.1	EST_HUMAN	X98107.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3159	8310	13470	3.52	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3287	8436	13597	0.82	9.2E-02	AA534354.1	EST_HUMAN	nt79e01.s1 NCI_CGAP_Oc3 Homo sapiens cDNA clone IMAGE:926136 3'
3573	8714		1.06	9.2E-02	6765215	NT	Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA
4216	9341		0.94	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4255	9407		0.76	9.2E-02	BE299722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980176 5'
4608	9726	14862	1.22	9.2E-02	X96402.1	NT	G.gallus Mla-CK gene
422	5209	10322	1.78	9.1E-02	X77655.1	NT	O. curticulus k12 keratin gene
2391	7497	12749	2.99	9.1E-02	P78986	SWISSPROT	G-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)
3847	8786		0.94	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161299-001-02 BT0349 Homo sapiens cDNA

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4463	9582	14720	1.35	9.1E-02	AL161654.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
743	5899	11052	5.28	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1645	6773	11965	4.26	9.0E-02	BE220482.1	EST_HUMAN	h039g10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element
2764	7858	13114	2.63	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2764	7858	13115	2.63	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3318	8465	13629	1.42	9.0E-02	AF279135.1	NT	Dicotyledonous dicotyledon spore coat structural protein SP65 (cotE) gene, complete cds
4275	9398	14538	0.61	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Salmir sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4275	9398	14539	0.61	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Salmir sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4396	9516	14658	0.97	9.0E-02	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
4638	9756	14903	2.02	9.0E-02	X65740.2	NT	Pleurothidium falciparum P-type ATPase 3 gene
1448	6576	11762	2.13	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1448	6576	11763	2.13	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
4171	9297		1.62	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds
4604	9722	14858	1.02	8.9E-02	AA424887.1	EST_HUMAN	2w03d04.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:768199 3'
1382	6510	11691	1.57	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3880	9016	14173	0.99	8.8E-02	AA239128.1	EST_HUMAN	EST11695 Uterus Homo sapiens cDNA 5' end
4008	9141		3.08	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII135) (TAFII-130) (TAFII130)
4217	9342		1.07	8.8E-02	4502804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4278	9401		0.76	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (enlidia, keratins) (PAX6), isoform b, mRNA
1659	6787	11982	1.11	8.7E-02	AI187281.1	EST_HUMAN	ox65b01.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1681161 3'
3670	8809	13966	4.16	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3670	8809	13967	4.16	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4674	9790	14936	1.39	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
1256	6385	11562	5.55	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2224	7336	12580	1.27	8.6E-02	BE408657.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3170	8321	13482	3.62	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (biub1) gene, complete cds

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3922	8761		3.68	8.6E-02	AF153362.1	NT	Dictyostellium discoideum adenyl cyclase (acaA) gene, complete cds
5135	10235	15371	2.2	8.6E-02	AF060174.1	NT	Rattus norvegicus synaptic vesicle protein 2C (SV2C) mRNA, complete cds
2373	7479	12733	1.4	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
2628	7947	12981	2.91	8.4E-02	W69330.1	EST_HUMAN	zd44e11.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
4331	9453	14587	0.95	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
4331	9453	14588	0.95	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
3579	8720	13878	6.98	8.3E-02	P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
1389	6517		4.18	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
1609	6936	11823	2.08	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAA74) mRNA, complete cds
3045	8199		2.21	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3780	8917		1.32	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3982	9116	14264	1.16	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4258	9383	14516	5.8	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4258	9383	14517	5.8	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4258	9383	14518	5.8	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5050	10152	15283	0.87	8.2E-02	AF240778.1	NT	Mus musculus peptinogen F (Pepf) mRNA, complete cds
5069	10167	15301	3.12	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (Znt-3) gene, complete cds
1508	6635	11822	1.14	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds
4931	10041	15180	0.66	8.1E-02	BF343921.1	EST_HUMAN	802015608F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4151640 6'
4931	10041	15181	0.66	8.1E-02	BF343921.1	EST_HUMAN	802015608F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4151640 5'
5	7881	10330	3.97	8.0E-02	AW954653.1	EST_HUMAN	EST356723 MAGE resequences, MAGE Homo sapiens cDNA
1713	7923	12042	8.36	8.0E-02	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1713	7923	12043	8.36	8.0E-02	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-16)
1809	7028	12248	3.28	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2446	7550		3.13	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2655	8019	13185	0.87	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3794	8931	14079	0.73	8.0E-02	AW966119.1	EST_HUMAN	EST1378191 MAGE resequences, MAGE Homo sapiens cDNA
4046	9177		0.66	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4743	9856	15004	1.19	8.0E-02	AK434202.1	EST_HUMAN	U31902.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132114 3'
4763	9896		6.97	8.0E-02	X72784.1	NT	M. musculus gene for gelatinase B
4898	10009	15154	0.65	8.0E-02	M28071.1	NT	Herpesvirus saimiri transformation-associated protein (STP), and dihydrofolate reductase (DHFR) gene, s complete cds, and small nuclear RNAs (lRNAs)
2153	7266	12516	1.91	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2959510 5'

Page 38 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2949	8103	13268	8.92	7.9E-02	AI582029.1	EST_HUMAN	ar98008.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876
3829	8955	14116	4.52	7.9E-02	6681044	NT	605 RIBOSOMAL PROTEIN L38 (HUMAN);
3829	8955	14117	4.52	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
4780	9803		1.37	7.9E-02	AB008019.1	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
4884	9995	15141	1.76	7.9E-02	L24757.1	NT	Arabidopsis thaliana RXW24L, mRNA, partial cds
4892	10003		4.93	7.9E-02	AW081738.1	EST_HUMAN	Human bone sialoprotein (BSP) gene, exons 2, 3 and 4
1213	6345	11514	1.42	7.8E-02	AI793275.1	EST_HUMAN	x570a10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581626 3'
1213	6345	11515	1.42	7.8E-02	AI793275.1	EST_HUMAN	oc59d02.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1 L3 L1
5071	8868		3.27	7.8E-02	BE250048.1	EST_HUMAN	repetitive element;
1406	7917	11712	1.02	7.7E-02	AF181897.1	NT	600843055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2959693 5'
3574	8715		1.89	7.7E-02	AJ230093.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3368	8513	13680	1.84	7.6E-02	BE514432.1	EST_HUMAN	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
3369	8533	13694	0.89	7.6E-02	AA2368447.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
785	5940	11098	1.54	7.5E-02	5902093	NT	EST112214 Cerebellum II Homo sapiens cDNA 5' and similar to similar to protocadherin 43
785	5940	11099	1.54	7.5E-02	5902093	NT	Homo sapiens solute carrier family 9 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1924	7043	12263	1.21	7.5E-02	AL163278.2	NT	Homo sapiens solute carrier family 9 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
477	5844	10785	1.44	7.4E-02	AW838547.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
1473	6800		1.1	7.4E-02	AF030027.1	NT	RC5-L1T0054-260100-011-H09 LT0054 Homo sapiens cDNA
2544	7847		1.03	7.4E-02	8755069	NT	Equine herpesvirus 4 strain NS80597, complete genome
3580	8721	13879	1.02	7.4E-02	AI807885.1	EST_HUMAN	Mus musculus paired-like homeodomain transcription factor 1 (Pbx1), mRNA
4672	9788	14933	1.11	7.4E-02	L78810.1	NT	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4763	9876	15027	2.6	7.4E-02	5978442	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4919	10029	15171	1.6	7.4E-02	8678492	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
468	5636	10775	1.3	7.3E-02	BE584961.2	EST_HUMAN	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchlp), mRNA
468	5636	10776	1.3	7.3E-02	BE584961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3688209 3'
883	5841	10980	3.42	7.3E-02	AE001789.1	NT	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3688209 3'
1491	7819	11808	3.35	7.3E-02	AW800281.1	EST_HUMAN	Thermotoga maritima section 101 of 136 of the complete genome
1856	7928		9.68	7.3E-02	AL163302.2	NT	CMO-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
4983	10091		1.11	7.3E-02	U12283.1	NT	Homo sapiens chromosome 21 segment HS21C102
							Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds

Page 39 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
116	5318	10460	0.97	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
116	5318	10461	0.97	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1486	6613	11800	2.02	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1486	6613	11801	2.02	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2520	7624		1.57	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
3862	8998	14155	0.64	7.2E-02	AW298322.1	EST_HUMAN	UI-H-BW0-ajl-a-05-0-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'
4323	9445	14578	5.25	7.2E-02	BF572307.1	EST_HUMAN	602077767F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251850 5'
1910	7029	12249	1.18	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2284	7374		1.21	7.1E-02	AE004890.1	NT	Pseudomonas aeruginosa PAO1, section 451 of 529 of the complete genome
2269	7379	12628	4.24	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
526	5892	10824	1	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1514	6641		1.12	7.0E-02	X96677.1	NT	Martellia Mbut-1 gene
3001	8166	13314	1.98	7.0E-02	AW138152.1	EST_HUMAN	UI-H-B11-acy-c-07-0-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3874	9010	14186	0.83	7.0E-02	AA815438.1	EST_HUMAN	ai65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:2716020 3'
4018	9151	14283	1.05	7.0E-02	BE070264.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4111	9239		0.82	7.0E-02	AW792962.1	EST_HUMAN	QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA
4188	9314	14449	1.07	7.0E-02	AF077821.1	NT	CMO-UM0001-000300-270-e12 UM0001 Homo sapiens cDNA
4907	10017	15161	7.25	7.0E-02	BF381987.1	EST_HUMAN	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
512	5678	10810	12.18	6.9E-02	AL163210.2	NT	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
512	5678	10811	12.18	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1338	6466		1.33	6.9E-02	4507968	NT	Homo sapiens chromosome 21 segment HS21C010
3770	8907	14059	1.06	6.9E-02	Q06364	SWISSPROT	Homo sapiens regulator of Gz-selective protein signalling (ZGAP1) mRNA, and translated products
3770	8907	14060	1.06	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
1912	7031	12251	2.62	6.8E-02	AF156873.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3075	8228	13379	1.13	6.8E-02	AA781996.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBCSR14) gene, complete cds
3075	8228	13380	1.13	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
3075	8228	13381	1.13	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
4528	9644		0.62	6.8E-02	BE141076.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1543	6671		1.63	6.7E-02	AF115536.1	NT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
1600	7019	12239	1.1	6.7E-02	A1220285.1	EST_HUMAN	hg78e04.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
3697	8635	13988	4.17	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOXD4 (CHOX-A)
1355	6484	11664	2	6.6E-02	A1735509.1	EST_HUMAN	at12e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to
2163	7276	12523	1.53	6.6E-02	AJ289241.1	NT	SW:LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
3445	8687	13750	8.96	6.6E-02	R64308.1	EST_HUMAN	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3459	8601	13765	2.55	6.6E-02	7108357	EST_HUMAN	y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3459	8601	13768	2.55	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4057	9187	14329	1.66	6.6E-02	AF200225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4963	10071	15207	9.79	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4963	10071	15208	9.79	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
580	5743	10871	1.8	6.5E-02	BF027638.1	EST_HUMAN	601671045f1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3964178 5'
988	6135	11305	2.02	6.5E-02	7706068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1398	6526	11705	3.1	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1748	6674	12079	1.22	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 96 of 109 of the complete genome
573	5737	10864	1.39	6.4E-02	X94649.1	NT	A. carterae precursor of peridrin-chlorophyll-a-protein (PCP) gene
1746	6872	12076	1.04	6.4E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
1746	6872	12077	1.04	6.4E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
4871	8140	13304	1.09	6.4E-02	6996923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
1766	6892	12089	2.36	6.3E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23,
3589	8729		2.12	6.3E-02	P37092	SWISSPROT	MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
4228	8363	14486	4.28	6.2E-02	AL161572.2	NT	HEAT SHOCK PROTEIN 70 HOMOLOG
4315	9437		1.88	6.2E-02	AF271235.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4556	9674		6.21	6.2E-02	Q62161	SWISSPROT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI1) mRNA, complete cds
253	5444	10583	3.71	6.1E-02	D16471.1	NT	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
3965	9101		2.78	6.1E-02	U73325.1	NT	Human mRNA, Xq terminal portion
4624	9742	14884	0.98	6.1E-02	AF119413.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKG1) gene, complete cds
4624	9742	14885	0.98	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
5152	10252	15391	28.79	6.1E-02	Y12503.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
1268	6395	11569	1.23	6.0E-02	AE001777.1	NT	S. scrofa mRNA for Man9-mannosidase
							Thermotoga maritima section 89 of 136 of the complete genome

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2637	7735	12989	1.12	6.0E-02	AW968848.1	EST_HUMAN	EST380924 IMAGE: ressequences, MAGJ Homo sapiens cDNA
2734	7828		1.27	6.0E-02	AB031289.1	NT	Mesocistidies corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2902	5302	10441	1.12	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.11 Stratiogene HeLa cell s3 937210 Homo sapiens cDNA clone IMAGE:626310 5'
2902	5302	10442	1.12	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.11 Stratiogene HeLa cell s3 937210 Homo sapiens cDNA clone IMAGE:626310 5'
3214	8365	13528	1.97	6.0E-02	AA372376.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3214	8365	13529	1.97	6.0E-02	AA372376.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
5081	10182	15319	4.4	6.0E-02	AF146738.1	NT	Rattus norvegicus testis specific protein mRNA, complete cds
228	5422	10559	4.39	5.9E-02	AW934719.1	EST_HUMAN	RC1-DT0001-290100-012-010 DT0001 Homo sapiens cDNA
2952	8106	13271	2.49	6.0E-02	AF190269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
5166	10264	15403	0.67	5.9E-02	AW028748.1	EST_HUMAN	ww34e02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
5166	10264	15404	0.67	5.9E-02	AW028748.1	EST_HUMAN	ww34e02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531460 3' similar to TR:O65386
934	6082	11997	4.76	5.8E-02	D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
1673	6802	11997	1.12	5.8E-02	Q61768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
3640	8779	13934	1.66	5.8E-02	AE001776.1	NT	Thermoboga maritima section 87 of 138 of the complete genome
4332	9454	14589	4.08	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4332	9454	14590	4.08	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4620	0638	14784	5.07	5.8E-02	AI247505.1	EST_HUMAN	ql56f01.x1 Soares_fetal_liver脾脾 INFILS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to db:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4520	9638	14785	5.07	5.8E-02	AI247505.1	EST_HUMAN	ql56f01.x1 Soares_fetal_liver脾脾 INFILS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to db:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4546	9684		2.31	5.8E-02	AF069264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
5155	10255	16394	0.63	5.8E-02	U76997.1	NT	Rattus norvegicus insulin-regulated membrane aminopeptidase (RAP) mRNA, complete cds
5198	10295	15432	1.41	5.8E-02	S66299.1	NT	growth hormone (Syrian Golden hamsters, mRNA, 809 nt)
3029	8183	13338	1.34	5.7E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611;
3043	8197	13353	1.42	5.7E-02	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3685	8824		0.73	5.7E-02	AF001282.1	NT	Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13RT), globin XI (ctt-12) and globin XI (ctt-11) genes, complete cds
3779	8816	14068	2.05	5.7E-02	AW966701.1	EST_HUMAN	EST378865 IMAGE: ressequences, MAGI Homo sapiens cDNA
1541	6669	11855	1.89	5.6E-02	AF094455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2265	7375		0.96	5.9E-02	BE904308.1	EST_HUMAN	601494578F2 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896610 5'
4610	9728	14884	1.2	5.0E-02	AB013100.1	NT	Lycopodium esculentum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4665	9781	14925	1	5.0E-02	AA280599.1	EST_HUMAN	zs45c01.st NC1 CGAP GC81 Homo sapiens cDNA clone IMAGE:700416 3'
2616	7714	12667	3.67	5.0E-02	X97869.1	NT	H. sapiens gene encoding La subunit
3200	8351	13514	4.24	5.0E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4190	9316	14450	1.05	5.0E-02	L41561.1	NT	Gallid herpesvirus mRNA fragment
1293	6422		2.32	5.4E-02	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
2991	8146		0.76	5.4E-02	AJ277468.1	NT	Oryza sativa rbb3-1 gene for putative Bowman Birk trypsin inhibitor
3403	10315		8.25	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
1055	6106	11360	1.75	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a03 ST0213 Homo sapiens cDNA
1055	6195	11361	1.75	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1521	6648	11835	3.37	5.3E-02	T94759.1	EST_HUMAN	ye37f12.1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01508
2468	7572	12825	1.3	5.3E-02	AJ276408.1	NT	Pseudomonas putida tgsS gene
2908	8062	13233	0.7	5.3E-02	M59417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
2908	8062	13234	0.7	5.3E-02	M59417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3131	8282	13438	4.27	5.3E-02	AJ276408.1	NT	Pseudomonas putida tgsS gene
5073	10174	15309	10.8	5.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
2261	7371		170.81	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3090	8243	13392	2.34	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3090	8243	13393	2.34	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3912	9048	14207	0.7	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Ord1) mRNA, complete cds
4252	9377	14508	3.63	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nsr-1 mRNA, complete cds
2344	7451		0.99	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D073 5'
4176	9302	14438	0.72	5.1E-02	AE001301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
482	5650	10788	1.14	6.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1207	6339	11509	14.54	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
1891	7108	12341	2.34	5.0E-02	P02810	SWISSPROT	4) (PIF-FIPF-S) (PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-3) (PRP-4) (PIF-FIPF-S) (PROLINE-RICH PHOSPHOPROTEIN C) (CONTAINS: PEPTIDE P-C)
2770	6134	11304	1.54	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3319	8466		1.4	5.0E-02	7305610	NT	Mus musculus Ubc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3581	8722		0.91	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3661	8800	13956	9.12	5.0E-02	U12769.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds



Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
222	5415		32.46	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
367	5547	10690	3.03	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
367	5547	10691	3.03	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2838	7993	13151	0.74	4.9E-02	U32036.1	NT	Zea mays phytoene synthase (Y1) gene, complete cds
3273	8422	13583	1.75	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)
3578	8719	13876	0.81	4.9E-02	AA400914.1	EST_HUMAN	2778a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3578	8719	13877	0.81	4.9E-02	AA400914.1	EST_HUMAN	2778a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4808	9920	15061	5.76	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2832386 3'
4808	9920	15062	5.76	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2832386 3'
5178	10273		1.34	4.9E-02	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
328	5512	10650	1.16	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
329	5512	10650	2.96	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
488	5656	10793	9.98	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2252	7362	12618	1.13	4.8E-02	W51983.1	EST_HUMAN	2c49b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3193	8344	13508	1.77	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4842	9760		1.05	4.8E-02	Z54280.1	NT	S. scrofa gene for skeletal muscle myosidine receptor
5109	10210	15347	0.81	4.8E-02	U91914.1	NT	Streptococcus constellatus D-alanine ligase gene, partial cds
4996	10102	15233	0.63	4.7E-02	6881261	NT	Rattus norvegicus Nestin (Nes), mRNA
268	5458	10598	2.47	4.6E-02	BE153583.1	EST_HUMAN	PMD-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
738	5894	11046	2.37	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1298	6425		0.98	4.6E-02	A1014255.1	EST_HUMAN	am50a002.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P80533
1368	6486	11679	2.37	4.6E-02	AV727059.1	EST_HUMAN	P90533 LIMA ;contains element LTR1 repetitive element ;
2462	7566	12819	1.62	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBW001 5'
2769	5458	10598	1.92	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1 ;
3477	8134	13287	0.82	4.6E-02	BE153583.1	EST_HUMAN	PMD-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
4095	9224		0.99	4.6E-02	AF220365.1	NT	PMD-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
446	5914	10760	2.56	4.5E-02	P22448	SWISSPROT	Mus musculus nuclear RNA helicase II(Gu (dtx21) gene, complete cds
1221	6353	11522	0.94	4.5E-02	AF005730.1	NT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1221	6353	11623	0.94	4.5E-02	AF005730.1	NT	Marburg virus strain MS Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1816	6339	12156	3.29	4.5E-02	P32182	SWISSPROT	Marburg virus strain MS Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
2100	7215	12462	2.27	4.5E-02	AE003984.1	NT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
							Xyella fastidiosa, section 110 of 229 of the complete genome

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3703	8841	13996	4.15	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
217	5411		3.43	4.4E-02	BE872733.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3936388 5'
1026	6167	11333	2.5	4.4E-02	L19295.1	NT	Drosophila melanogaster extracellular (EXD) mRNA, complete cds
2087	7203		1.94	4.4E-02	P31588	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2463	7567	12820	1.02	4.4E-02	AW875475.1	EST_HUMAN	QV2-P10012-010300-070-002 PT0012 Homo sapiens cDNA
3618	8767	13913	1.99	4.4E-02	AF159160.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4596	9714	14850	1.03	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4596	9714	14851	1.03	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
781	5936	11094	6.56	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
3411	8654	13713	8.36	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3636	8775		1	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
823	5976	11140	1.39	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
867	6018		1.91	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
897	6047	11218	0.73	4.2E-02	AW003645.1	EST_HUMAN	L1 RETROPOSOM, ORF2 MRNA ;contains L1.13 L1 L1 repetitive element ;
1734	6861		2.36	4.2E-02	AL445066.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
1786	6914	12121	1.13	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3641	8780	13935	2.72	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4151	9570		7.38	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-164-066 NN0012 Homo sapiens cDNA
3226	8378	13539	4.02	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3777	8914	14066	1.05	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
1121	6259	11424	2.96	3.9E-02	BF516149.1	EST_HUMAN	U1-H-BW1-enc-h-08-Q-U1.s1 NCL_CGAP_Sub57 Homo sapiens cDNA clone IMAGE:3084134 3'
1351	6480	11659	2.91	3.8E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1965	7082	12306	1.5	3.9E-02	AJ403386.1	NT	Musculus DNA for desmin-binding fragment DesD7
2685	7761		1.76	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
4110	9238	14375	1.12	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
4110	9238	14376	1.12	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5119	10200	15354	0.61	3.9E-02	AW392417.1	EST_HUMAN	RC6-ST0258-171199-021-C09 ST0258 Homo sapiens cDNA
5139	10239	15376	1.02	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5139	10239	15376	1.02	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
2110	7225		0.97	3.8E-02	AJ251973.1	NT	Homo sapiens partial steerin-1 gene

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4808	10016	15160	0.98	3.8E-02	AU124122.1	EST_HUMAN	AU124122.NT2RM2 Homo sapiens cDNA clone NT2RM2007698 5'
993	6139	11308	4.31	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2218	7330	12883	3.72	3.7E-02	A1984806.1	EST_HUMAN	wf65e08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
3022	8176	13333	1.21	3.7E-02	P79944	SWISSPROT	ECOMESODERMIN
3024	8178	13334	5.36	3.7E-02	BF312963.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126584 5'
3436	8578		1.05	3.7E-02	6860541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcma3), mRNA
3171	8322	13483	1.38	3.6E-02	AP000003.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 644001-777000 nt. position (3/7)
3631	8770	13928	0.77	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3639	8778	13933	0.65	3.6E-02	AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
898	6048	11217	1.41	3.5E-02	U09506.1	NT	Drosophila melanogaster liggrin mRNA, complete cds
1009	6153	11320	1.03	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1579	6708	11898	1.37	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4249377 5'
1579	6708	11899	1.37	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4249377 5'
4187	9313	14448	1.83	3.5E-02	AE001773.1	NT	Thermotoga maritima section 86 of 136 of the complete genome
4293	9415	14550	1.15	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
5177	10274		0.97	3.5E-02	P47144	SWISSPROT	HYPOTHETICAL 80.7 KD PROTEIN IN SOD1-GPA2 INTERGENIC REGION
576	5740	10867	1.05	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
576	5740	10868	1.05	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
577	5740	10867	4.5	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
577	5740	10868	4.5	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1053	6194	11358	3.17	3.4E-02	AW274020.1	EST_HUMAN	xv26d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW: C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR;
1209	6341		8.4	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2369	7475	12729	1.38	3.4E-02	T57160.1	EST_HUMAN	yc20e06.r1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3412	8555	13714	1.18	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3756	8893	14043	0.85	3.4E-02	BE639514.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
3894	9030	14189	3.8	3.4E-02	AW794952.1	EST_HUMAN	RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4571	9889	14827	2.46	3.4E-02	X59709.1	NT	M. musculus S-antigen gene promoter region
5042	10144		2.25	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5061	10163	15286	1.48	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
370	5550		21.45	3.3E-02	AA398735.1	EST_HUMAN	z75603.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1169	6304	11470	9.4	3.3E-02	AB035867.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1650	6778	11870	1.49	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds
2077	7193		1.25	3.3E-02	R09112.1	EST_HUMAN	y2509.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:127888 5'
2426	7532	12785	0.95	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
3342	8488	13654	1.16	3.3E-02	H02399.1	EST_HUMAN	y35h02.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:150771 5'
4148	8778	11870	2.58	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds
4446	9565	14707	2.2	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
4778	9892	15039	0.53	3.3E-02	AW276696.1	EST_HUMAN	xp-0004.x1 NCJ CGAP_HN11 Homo sapiens cDNA clone IMAGE:2742799 3'
127	5325	10471	1.73	3.2E-02	AJ002005.1	NT	Oryzobagrus curticulus gene encoding ileal sodium-dependent bile acid transporter
1127	6264	11428	15.01	3.2E-02	AF066275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1127	6284	11429	15.01	3.2E-02	AF066275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2108	7223		2.07	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
2802	5325	10471	0.53	3.2E-02	AJ002005.1	NT	Oryzobagrus curticulus gene encoding ileal sodium-dependent bile acid transporter
3112	8265	13420	9.38	3.2E-02	BE867353.1	EST_HUMAN	601442431.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3846727 5'
3693	8831	13986	1.21	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
3933	9099	14224	0.66	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
3933	9099	14225	0.66	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
4194	9319		14.19	3.2E-02	X94768.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4733	9846	14992	3.38	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
4924	10034		1.54	3.2E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
1264	6393		2.27	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1309	6439	11615	1.45	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1976	7093		1.31	3.1E-02	Z50097.1	NT	Drosophila melanogaster mRNA for headcase protein
1635	6764		2.14	3.0E-02	AF187125.1	NT	Pityokines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
3552	8693	13855	1.07	3.0E-02	M04176.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSI.2 gene, complete cds
3630	8789	13925	2.46	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3726	8863		0.82	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0296-150200-040-009 ST0296 Homo sapiens cDNA
3920	9066		1.08	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA 5' end
4661	9777		12.98	3.0E-02	A1240467.1	EST_HUMAN	qh10g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844314 3'
5032	10134	15264	6.62	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced

Page 47 of 214  
Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5032	10134	15265	6.62	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3546	8887	13850	0.77	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
3903	9039	14199	0.71	2.9E-02	H72805.1	EST_HUMAN	y007e10.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:233130 5'
3958	9093	14245	1.34	2.9E-02	O15440	SWISSPROT	MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 5 (ABC TRANSPORTER MOAT-O) (PABC11)
564	5729		0.64	2.8E-02	AW970153.1	EST_HUMAN	(SMRP)
3349	8494	13661	1.12	2.8E-02	AF068063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3349	8494	13662	1.12	2.8E-02	AF068063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4289	9411		0.77	2.8E-02	8383751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1499	6626	11813	1.13	2.7E-02	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
3413	8556	13715	1.71	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4174	9300	14435	1.88	2.7E-02	N47258.1	EST_HUMAN	y66h12.r1 Soares_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:280487 5'
4174	9300	14436	1.88	2.7E-02	N47258.1	EST_HUMAN	y66h12.r1 Soares_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:280487 5'
570	5734	10862	0.94	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1377	6505		1.09	2.6E-02	AW850515.1	EST_HUMAN	IL3-CT0219-280100-062-C09 CT0219 Homo sapiens cDNA
2346	7453	12706	1.53	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2348	7455	12709	2.45	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2881	8035		1.28	2.6E-02	AF109806.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, end smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
3937	9073		0.96	2.6E-02	AW181945.1	EST_HUMAN	x66f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2662409 3'
4878	9989	15135	2.43	2.6E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
5047	10149	15279	1.7	2.6E-02	AE002014.1	NT	Delinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5077	10178	15313	1.95	2.6E-02	AW241154.1	EST_HUMAN	xa52b04.x1 NCI_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069
530	5696	10828	1.62	2.5E-02	AI793130.1	EST_HUMAN	on26f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
530	5696	10829	1.62	2.5E-02	AI793130.1	EST_HUMAN	on26f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
810	5963	11125	14.46	2.5E-02	BE974314.1	EST_HUMAN	G01680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865 3'
870	6021	11192	4.53	2.5E-02	BE974314.1	EST_HUMAN	G01680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865 3'
2724	7819		2.23	2.5E-02	U12571.1	NT	Rattus norvegicus rebphilin-3A mRNA, complete cds
2923	8077	13245	3.22	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1

Page 48 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2923	8077	13246	3.22	2.5E-02	X99897.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4018	10308	14294	0.93	2.5E-02	BE701185.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4018	10308	14295	0.93	2.5E-02	BE701185.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4178	9304	14439	5.14	2.5E-02	AW592114.1	EST_HUMAN	h36h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5083	10312		11.72	2.5E-02	AI754201.1	EST_HUMAN	cr21f11.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_cr21f11 3'
169	5364	10506	0.63	2.4E-02	AI378592.1	EST_HUMAN	lc72c07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2070186 3'
1611	6739	11933	1.86	2.4E-02	H65884.1	EST_HUMAN	y75f11.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:211149 5'
2038	7931	12395	0.98	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2038	7931	12396	0.96	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4347	9489	14606	1.59	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TGBP 25) protein mRNA, complete cds
4495	9614	14754	1.33	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4495	9614	14755	1.33	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5175	10272		1.2	2.4E-02	AF134513.1	NT	Kadipiro virus segment 6 VP6 gene, complete cds
1882	7002		2.4	2.3E-02	W03340.1	EST_HUMAN	z884g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:289294 5'
1895	7014		3.49	2.3E-02	U84165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2330	7437	12690	1.36	2.3E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF_YDL245c
3659	8798	13954	6.18	2.3E-02	Z20377.1	EST_HUMAN	HSAAAACADHP, Human fetal Brain Whole tissue Homo sapiens cDNA
3694	8832		2.23	2.3E-02	L23429.1	NT	Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3' end
4121	9249	14386	0.69	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4121	9249	14387	0.69	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4398	9518	14659	1.03	2.3E-02	AW89107.1	EST_HUMAN	GM4-NN0080-280400-160-504 NN0080 Homo sapiens cDNA
4427	9547	14685	0.9	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4427	9547	14687	0.9	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4428	10309	14688	0.75	2.3E-02	AW593983.1	EST_HUMAN	xe25608.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4428	10309	14689	0.75	2.3E-02	AW593983.1	EST_HUMAN	xe25608.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4567	9885	14824	2.62	2.3E-02	BF026487.1	EST_HUMAN	60167279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4567	9885	14825	2.62	2.3E-02	BF026487.1	EST_HUMAN	60167279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5132	10232	15367	0.78	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5132	10232	15368	0.78	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
736	5892	11044	2.95	2.2E-02	AF018267.1	NT	Columba livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1759	6885		1.44	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1772	6898	12105	1.12	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1772	6898	12106	1.12	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2011	7128	12365	1.12	2.2E-02	Z82001.1	NT	S.pneumoniae pcpA gene and open reading frames
3416	8559		1.84	2.2E-02	AA577786.1	EST_HUMAN	nm24e04.s1 NCI_CGAP_Gast1 Homo sapiens cDNA clone IMAGE:1084782 3'
3824	8763		4.07	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3832	8868	14122	1.16	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3893	9028	14188	0.88	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4585	9703		1.38	2.2E-02	P18759	SWISSPROT	HYPOTHETICAL PROTEIN UL21
5048	10150	15280	0.92	2.2E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
5172	9029	14188	2.31	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
418	5586		4.02	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
448	5516		6.76	2.1E-02	AF028726.1	NT	Dictyostellium discoideum histidine kinase C (dhkC) mRNA, complete cds
1267	6396	11570	6.19	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), ColL (cotL), and spore coat protein ColM (cotM) genes, complete cds
1792	6918	12126	1.15	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1792	6918	12127	1.15	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1792	6918	12128	1.15	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2177	5934	11092	3.07	2.1E-02	N29266.1	EST_HUMAN	yx43h07.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264541 5'
3128	7146	12386	4.64	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0348-120100-001-f11 BT0548 Homo sapiens cDNA
3128	7146	12387	4.84	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
3571	8712	13872	1.16	2.1E-02	AA461271.1	EST_HUMAN	zx63b09.r1 Soares_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:798121 5'
4102	9231	14368	0.6	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4286	8408	14644	0.7	2.1E-02	BF343655.1	EST_HUMAN	602015306F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4151161 5'
4423	8543	14982	1.79	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
4433	8852	14895	1.33	2.1E-02	A1769127.1	EST_HUMAN	wg81d11.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4472	8691		15.42	2.1E-02	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
4849	8591		1.54	2.1E-02	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
4877	8793	14939	4.85	2.1E-02	Z08501.1	NT	A.thaliana mitochondrial genome, part A
4698	8814	14962	0.72	2.1E-02	AA686737.1	EST_HUMAN	ag55g12.s1 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4788	8901	15042	0.67	2.1E-02	A1823432.1	EST_HUMAN	wh54a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
17	5228	10340	1.16	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.3
18	5229	10341	7.52	2.0E-02	AW895665.1	EST_HUMAN	MER1 repetitive element;
258	5447	10595	2.69	2.0E-02	6753635	NT	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
293	5481	10823	2.38	2.0E-02	AA456538.1	EST_HUMAN	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
769	5953	11113	1.41	2.0E-02	6753635	NT	aa15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
							Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA

Page 50 of 214  
Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1088	6227	11392	1.21	2.0E-02	AL098805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1(p36.33) of Homo sapiens
1202	6335	11505	1.33	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1202	6335	11506	1.33	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1883	7003	12221	1.29	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1883	7003	12222	1.29	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2769	7863		2.22	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3051	5228	10340	1.17	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1:13
3122	8274		1.44	2.0E-02	7305474	NT	MER1 repetitive element;
3212	8363		1.28	2.0E-02	AF005588.1	NT	Mus musculus sem domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3981	9115	14263	1.19	2.0E-02	M18095.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
5093	10193		2.7	2.0E-02	A1271995.1	EST_HUMAN	P_vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
691	5848	10991	1.77	1.9E-02	AA572764.1	EST_HUMAN	q83c03.x1 NCI_CGAP_K163 Homo sapiens cDNA clone IMAGE:1866076 3'
1628	6757	11851	0.85	1.9E-02	P18488	SWISSPROT	trf19a07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.1 L1 repetitive element;
2033	7151	12390	1.63	1.9E-02	AL163303.2	NT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2033	7151	12391	1.63	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2870	8024	13190	7.47	1.9E-02	AA713856.1	EST_HUMAN	rm04f05.s1 NCI_CGAP_SST Homo sapiens cDNA clone IMAGE:1288337 3'
2919	8073	13243	1.57	1.9E-02	AV048669.1	EST_HUMAN	AV048669 GLC Homo sapiens cDNA clone GLOBLH07 3'
3656	8734		1.05	1.9E-02	N52250.1	EST_HUMAN	YZ28b02.s1 Soares_multiple sclerosis_2N6HMSP Homo sapiens cDNA clone IMAGE:284331 3'
3681	8820		9.11	1.9E-02	BE738088.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
3695	8833	13987	0.72	1.9E-02	AI301183.1	EST_HUMAN	qr04c07.x1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element;
4021	9193	14297	1.39	1.9E-02	AF141940.1	NT	Mycoplasma imitans VHA1 precursor (VHA1) and VHA2 precursor (VHA2) genes, partial cds
4165	9291	14428	1.59	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4165	9291	14429	1.59	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4514	9632	14777	2.89	1.9E-02	AI452999.1	EST_HUMAN	tf46d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
4999	7581	12832	2.69	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
343	5626	10682	2.13	1.9E-02	AW771104.1	EST_HUMAN	hm52c06.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
1182	6297	11463	1.42	1.8E-02	X17664.1	NT	MER29 repetitive element;
							H.francisci mRNA for myelin basic protein (MBP)



Page 51 of 214  
Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2640	7738	12991	1.26	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3195	8346		0.98	1.8E-02	AI805929.1	EST_HUMAN	test2a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090286 3'
4063	9194		1.06	1.8E-02	AA661446.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4408	9528	14688	1.25	1.8E-02	AW936383.1	EST_HUMAN	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
907	6057	11226	1.22	1.7E-02	BE394869.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1801	6926	12138	1.37	1.7E-02	AW573183.1	EST_HUMAN	ht34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element;
1801	6926	12139	1.37	1.7E-02	AW573183.1	EST_HUMAN	ht34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element;
1881	7001		1.44	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2102	7217		5.4	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsuguin29, complete cds
2966	8120	13284	1	1.7E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3497	8638		4.29	1.7E-02	AW827368.1	EST_HUMAN	hm45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;
4140	9288		1.01	1.7E-02	AA669818.1	EST_HUMAN	act19f04.s1 Strelagene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element/contains element MER24 repetitive element;
4172	9298		2.34	1.7E-02	RO2506.1	EST_HUMAN	ye86f08.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:124947 5'
4432	9551	14694	0.62	1.7E-02	AI305279.1	EST_HUMAN	qm08g07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb.X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4502	9621	14763	1.68	1.7E-02	AW573183.1	EST_HUMAN	ht34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element;
4582	9798	14943	2.08	1.7E-02	V00541.1	NT	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
4782	9895		5.03	1.7E-02	AI015076.1	EST_HUMAN	ov81e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640888 3'
5153	10253	15392	0.62	1.7E-02	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
510	5676		1.55	1.6E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 13/162
1689	6798	11994	0.98	1.6E-02	Y18889.1	NT	Treponema mallophilum flaB2, flaB3 and flilD genes for flagellin subunit proteins and CAP protein homologue
2230	7342	12595	1.45	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2230	7342	12596	1.45	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2606	7705	12961	1.4	1.6E-02	AA454872.1	EST_HUMAN	nc81d06.c1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2655	7763		1.13	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
2989	8144	13306	0.66	1.6E-02	AF112282.1	NT	Laccase sp. isolate 1Bd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3512	8653	13619	4.35	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3828	8962	14112	0.91	1.0E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
4146	9274		2.14	1.0E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4276	9399	14540	1.02	1.0E-02	AW875407.1	EST_HUMAN	QV2-P10012-140100-030-407 P10012 Homo sapiens cDNA
750	5906		33.34	1.0E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2127	7241	12483	1.83	1.0E-02	N39521.1	EST_HUMAN	y27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
2164	7267	12516	1.33	1.0E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3033	8187	13342	1.72	1.0E-02	AJ006216.1	NT	Homo sapiens CAGNATF gene, exons 1 to 48
3033	8187	13343	1.72	1.0E-02	AJ006216.1	NT	Homo sapiens CAGNATF gene, exons 1 to 48
3705	8843	13998	0.9	1.0E-02	BF092042.1	EST_HUMAN	NR4-TN0115-080900-201-512 TN0115 Homo sapiens cDNA
416	5584		1.44	1.0E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1119	6257	11421	3.44	1.0E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1260	6389		2.71	1.0E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1302	6492		2.7	1.0E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1403	6531		2.39	1.0E-02	AF216854.1	NT	Homo sapiens headpin gene, complete cds
1532	6659		0.97	1.0E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'
3197	8348	13510	2.4	1.0E-02	AF160969.2	NT	Blifidobacterium longum Nav/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (agIL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xyR) gene, partial cds
3370	8524	13687	0.67	1.0E-02	AW074212.1	EST_HUMAN	x609d09.xt NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2575793 3'
3466	8608	13772	5.95	1.0E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3466	8608	13773	5.95	1.0E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3505	8846	13812	1.17	1.0E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3633	8772	13928	7.72	1.0E-02	698918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4466	9585	14723	6.9	1.0E-02	AW962888.1	EST_HUMAN	EST374761 IMAGE resequences; MAGG Homo sapiens cDNA
4466	9585	14724	6.9	1.0E-02	AW962888.1	EST_HUMAN	EST374761 IMAGE resequences; MAGG Homo sapiens cDNA
4847	9959	15102	6.95	1.0E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4847	9959	15103	6.95	1.0E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
1876	6996		0.98	1.0E-02	BF739263.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828335 5'
1959	7076	12299	1.32	1.0E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C001
3198	8349	13511	1.97	1.0E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3198	8349	13512	1.97	1.0E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3942	9078		1.27	1.0E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
210	5404		0.71	1.2E-02	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
352	5534	10873	3.3	1.2E-02	AA059299.1	EST_HUMAN	z66g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
452	5820	10763	2.68	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
737	5893	11045	0.77	1.2E-02	A183522.1	EST_HUMAN	q68e12.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.L1 L1 repetitive element;
2157	7270	12518	1.14	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2160	7273	12521	1.21	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2420	7525	12778	0.97	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2457	7561	12813	1.27	1.2E-02	AL163216.2	NT	Homo sapiens chromosome 21 segment HS21C018
3076	8229	13582	6.89	1.2E-02	AA075418.1	EST_HUMAN	z188e03.r1 StrataGene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3272	8421	13582	1.85	1.2E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
4852	9964	15109	0.99	1.2E-02	6754367	NT	Mus musculus interferon regulatory factor 5 (Irf5), mRNA
4893	10004	15148	1.99	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoKet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5024	10126		1.27	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CplbiqT mRNA, partial cds
5088	10170	15305	1.77	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
1273	6402	11576	1.05	1.1E-02	AA070364.1	EST_HUMAN	z188e11.s1 StrataGene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1721	6848	12052	1.35	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1721	6848	12053	1.35	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2032	7150	12389	2.99	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153808 5'
2843	7998		3.8	1.1E-02	N69523.1	EST_HUMAN	z440e05.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:295040 5'
3509	8650	13817	2.28	1.1E-02	A1653508.1	EST_HUMAN	tg95b10.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN
4082	9211		0.64	1.1E-02	AW813796.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4798	9911	15052	2.21	1.1E-02	AL049383.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
6	5217	10331	7.57	1.0E-02	AW846120.1	EST_HUMAN	DKFZp566E0924_s1 588 (synonym: hube1) Homo sapiens cDNA clone DKFZp566E0924
3062	8215	13369	2.62	1.0E-02	BE83556.1	EST_HUMAN	MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA
3245	8395	13557	1.16	1.0E-02	BE068999.1	EST_HUMAN	RC0-FN0025-250500-021-002 FN0025 Homo sapiens cDNA
3493	8634		0.64	1.0E-02	AW845621.1	EST_HUMAN	601649667R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
3859	8995	14152	0.78	1.0E-02	A1655086.1	EST_HUMAN	MR0-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA
4744	9857	15005	4.26	1.0E-02	6753521	NT	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
							Mus musculus corticotropin releasing hormone receptor 2 (Cnr2), mRNA

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4813	9825	15066	5.66	1.0E-02	R96567.1	EST_HUMAN	y454h01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5'
894	6044	11215	3.28	9.0E-03	A1796126.1	EST_HUMAN	wh4209.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1268	6397		1.47	9.0E-03	BE781889.1	EST_HUMAN	MER22 MER22 repetitive element;
1490	6618	11807	1.58	9.0E-03	AE001270.1	NT	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2372	7478	12732	1.4	9.0E-03	AL161559.2	NT	Treponema pallidum section 86 of 87 of the complete genome
2871	8025	13191	0.8	9.0E-03	A1251744.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2871	8025	13192	0.8	9.0E-03	A1251744.1	EST_HUMAN	q180f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3645	8784	13936	0.62	9.0E-03	J05184.1	NT	q180f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
4972	10080	15217	1.14	9.0E-03	BE047949.1	EST_HUMAN	S.acidocaldarius thermopsis gene, complete cds
							tz44e10.y1 NCI_CGAP_Brm62 Homo sapiens cDNA clone IMAGE:2291466 5'
501	5688		2.57	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.s1 Soares_pinea_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains
980	6137	11306	83.35	8.0E-03	AF106656.1	NT	Alu repetitive element;
2140	7254	12500	1	8.0E-03	AL163283.2	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
							Homo sapiens chromosome 21 segment HS21C083
2928	8092		0.97	8.0E-03	U47048.1	NT	Escherichia coli microcin 24 region, DNA binding protein (mdbA), immunity protein (mtfI), microcin 24 (mtfS), and microcin transport protein (mtfA, mtfB) genes, complete cds
3340	8486	13652	0.8	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3653	8792	13947	1.28	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3653	8792	13948	1.28	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4362	9484	14625	4.21	8.0E-03	BF363327.1	EST_HUMAN	Gm4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
6164	10264	16303	0.94	8.0E-03	U02970.1	NT	Protheca wickerhamii 263-11 complete mitochondrial DNA
692	5849	10892	12.77	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
692	5849	10893	12.77	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
978	6124	11294	5.37	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1117	6255	11419	2.78	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
							FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1373	6501		1.02	7.0E-03	Q61060	SWISSPROT	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HFH-2)
1402	6530	11709	3.16	7.0E-03	AA668298.1	EST_HUMAN	ab79b09.s1 Stragelene fetal retina G37202 Homo sapiens cDNA clone IMAGE:853145 3'
1517	6644	11830	2.52	7.0E-03	AW303599.1	EST_HUMAN	xx21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
1763	6879	12084	1.23	7.0E-03	AW950556.1	EST_HUMAN	EST3362626 IMAGE ressequences, MAGA Homo sapiens cDNA
1763	6879	12085	1.23	7.0E-03	AW950556.1	EST_HUMAN	EST3362626 IMAGE ressequences, MAGA Homo sapiens cDNA
2236	7936	12606	1.36	7.0E-03	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3544	8895	13847	0.73	7.0E-03	A150273.1	EST_HUMAN	qf34h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1761955 3'
3747	8895	14036	0.72	7.0E-03	AW444463.1	EST_HUMAN	UI-H-B13-alk-c-10-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3789	8926	14076	0.96	7.0E-03	AF198344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4572	9690		1.42	7.0E-03	AW630888.1	EST_HUMAN	h189a05.y1 NC1_CGAP_GUT Homo sapiens cDNA clone IMAGE:296936 5'
4974	10082		2.18	7.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5086	10186	15324	1.02	7.0E-03	BE044191.1	EST_HUMAN	h30h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:O93434
5086	10186	15325	1.02	7.0E-03	BE044191.1	EST_HUMAN	O93434 RETICULOCALBIN ;
1244	6375	11560	9.29	6.0E-03	AW511148.1	EST_HUMAN	h39h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:O93434
1244	6375	11551	9.29	6.0E-03	AW511148.1	EST_HUMAN	h39h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXN_HUMAN O75489 ORPHAN NUCLEAR RECEPTOR PXR ;
2857	8012	13174	1.7	6.0E-03	AA759135.1	EST_HUMAN	h22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to h22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXN_HUMAN O75489 ORPHAN NUCLEAR RECEPTOR PXR ;
2857	8012	13175	1.7	6.0E-03	AA759135.1	EST_HUMAN	h22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to h22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXN_HUMAN O75489 ORPHAN NUCLEAR RECEPTOR PXR ;
3229	8379		2.39	6.0E-03	HT5680.1	EST_HUMAN	h78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
3286	8435		1.13	6.0E-03	AF190338.1	NT	h77h04.r1 Soares_fetal liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3363	8508	13675	1.21	6.0E-03	U90880.1	NT	Neotoma sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3363	8508	13675	1.21	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3363	8508	13675	1.21	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3533	8675	13931	1.12	6.0E-03	W37086.1	EST_HUMAN	zcl3a11.r1 Soares_papillary tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3637	8776	13931	4.08	6.0E-03	BF510986.1	EST_HUMAN	UI-HB14-apm-c-06-0-UI.s1 NC1_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087764 3'
3671	8810	13988	0.92	6.0E-03	BE077358.1	EST_HUMAN	RC1-BT0606-260400-014-a07 BT0606 Homo sapiens cDNA
3758	8835	14045	1.2	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
3896	9032	14192	1.21	6.0E-03	AW847284.1	EST_HUMAN	RC0-CT0204-240989-021-510 CT0204 Homo sapiens cDNA
3929	9065		0.8	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5'
4342	9484		2.01	6.0E-03	AI016833.1	EST_HUMAN	ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4604	9790	14924	8.05	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
668	5828	10967	1.88	5.0E-03	L25105.1	NT	Gliamylia trachomatis partial ORF8; aminocacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
668	5828	10968	1.88	5.0E-03	L25105.1	NT	Gliamylia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
669	5828	10967	2.65	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
669	5828	10968	2.65	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1113	6251	11415	0.99	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
2642	7740	12993	1.64	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2901	8055	13224	0.75	5.0E-03	BE260057.1	EST_HUMAN	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538789 5'
3114	8267	13423	3.72	5.0E-03	T87623.1	EST_HUMAN	yc8109.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3133	8284		2.08	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3145	8296	13455	1.14	5.0E-03	R71794.1	EST_HUMAN	y86g02.s1 Soares breast 2N1B-Het Homo sapiens cDNA clone IMAGE:155666 3'
3261	8410		0.99	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3676	8816	13971	3.63	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (pbpB) gene, complete cds
3739	8877	14028	0.7	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
3944	9080		1.49	5.0E-03	AA298876.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4281	9404	14543	0.65	5.0E-03	H78356.1	EST_HUMAN	yJ79g10.r1 Soares fetal liver spleen 1N1B Homo sapiens cDNA clone IMAGE:240086 5'
4283	8877	14028	0.77	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4580	9688	14835	1.3	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4687	9803	14950	1.53	5.0E-03	AJ762387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn15c02 random
231	5425	10563	8.16	4.0E-03	AW500196.1	EST_HUMAN	UI-HF-BNO-akc-h-04-0-UL.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
319	5505	10543	1.71	4.0E-03	R48482.1	EST_HUMAN	y851e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
442	5610	10756	0.82	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
601	5763	10891	4.31	4.0E-03	AA939339.1	EST_HUMAN	cn75g12.s1 Soares NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:1562566 3'
878	6028	11201	1.78	4.0E-03	R48482.1	EST_HUMAN	y851e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
912	6082		3.34	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT03333-110100-012-101 BT0333 Homo sapiens cDNA
1152	6288	11453	23.83	4.0E-03	AA099777.1	EST_HUMAN	z81a08.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:510998 5'
1171	6306	11473	1.43	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1307	6437	11612	1.15	4.0E-03	AA284374.1	EST_HUMAN	zs59a01.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1599	6727		1.29	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB03 5'
1755	6881	12087	2.25	4.0E-03	U39472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds
2013	7130	12368	5.61	4.0E-03	AA099777.1	EST_HUMAN	z81a08.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:510998 5'
2228	7340		1.6	4.0E-03	BE410556.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2255	7366	12821	1.19	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2537	7640	12888	1.09	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
2537	7640	12889	1.09	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
2652	7750	12999	2.57	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2652	7750	13000	2.57	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2657	7764	13003	1.11	4.0E-03	AL163294.2	NT	Homo sapiens chromosome 21 segment HS21C084
3210	8361	13523	1.16	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3210	8361	13524	1.16	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3517	8658	13824	0.74	4.0E-03	AW188426.1	EST_HUMAN	X88104.X1 NCL CGAP Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3517	8658	13825	0.74	4.0E-03	AW188426.1	EST_HUMAN	X88104.X1 NCL CGAP Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3970	9104		1.84	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
5187	10284		1.19	4.0E-03	O98821	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
369	5549	10693	2.01	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
880	6030	11202	11.35	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1674	6903	11698	3.31	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCL CGAP Pr2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2270	7380		4.86	3.0E-03	Z32521.1	NT	S. cereale (cv. Halo) mRNA for triosephosphate isomerase
2861	8115		1.75	3.0E-03	Y09006.1	NT	Arabidopsis thaliana rpoM1 gene
3055	8208	13363	4.44	3.0E-03	BE379296.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3130	8281	13437	2.82	3.0E-03	AW802887.1	EST_HUMAN	IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3399	8543	13702	1.58	3.0E-03	U94608.1	NT	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 1 and 2
3408	8551		7.13	3.0E-03	Y12500.1	NT	C. elegans samde gene
3950	9085	14239	5.93	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBG01 5'
3950	9085	14240	5.93	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBG01 5'
4011	9144	14284	1.37	3.0E-03	AI792278.1	EST_HUMAN	ar04f08.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155989 5'
4122	9250		1.24	3.0E-03	Z32521.1	NT	S. cereale (cv. Halo) mRNA for triosephosphate isomerase
4374	9495	14639	13.02	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4492	9811	14751	4.98	3.0E-03	AI536141.1	EST_HUMAN	xu8.P10.H3 conorm Homo sapiens cDNA 3'
4801	9914	15055	3.48	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4823	9935	15076	7.71	3.0E-03	BE787945.1	EST_HUMAN	601482175F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5123	10224	15359	1	3.0E-03	4508414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GAI) mRNA
5123	10224	15360	1	3.0E-03	4508414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GAI) mRNA
5159	10259	15398	0.92	3.0E-03	S52213.1	NT	CD11b-leukocyte integrin alpha chain [human, Genomic, 104 nt, segment 23 of 31]
5174	10271	15412	1.32	3.0E-03	AW237794.1	EST_HUMAN	hm81c09.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2860608 3'
513	5679	10812	0.77	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
513	5679	10813	0.77	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
766	7901		10.76	2.0E-03	T70874.1	EST_HUMAN	yd15h03.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108341 5'
1372	6500	11683	2.08	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1376	6503	11685	1.9	2.0E-03	AA661605.1	EST_HUMAN	nu86f01.s1 NC1_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217593
1384	6512	11693	5.44	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1500	6827	11814	1.55	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1531	6858	11844	1.76	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1531	6858	11845	1.76	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1604	6732		5.07	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR
1781	6907	12116	1.08	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares total_fetus_Nb2-IF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1986	7113	12348	1.27	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2543	7646		4.07	2.0E-03	AW137762.1	EST_HUMAN	UI-H-B11-edl-g-10-o-UJ.s1 NC1_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3398	8542	13701	3.39	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares total_fetus_Nb2-IF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3404	8547	13706	0.98	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3643	8782	13936	5.49	2.0E-03	X87344.1	NT	H.sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4089	9217	14353	1.66	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4197	9322		9.07	2.0E-03	U08491.1	NT	Rattus norvegicus 5-hydroxytryptamine/ receptor gene, partial cds
4405	9525		0.96	2.0E-03	AW297380.1	EST_HUMAN	UI-H-BW0-ali-g-03-0-UJ.s1 NC1_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4519	9637	14792	2.13	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4519	9637	14793	2.13	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4678	9794		1.47	2.0E-03	R07773.1	EST_HUMAN	yo45e02.s1 Soares adult brain N2b-4HB5Y Homo sapiens cDNA clone IMAGE:180890 3'
5005	10110	15239	0.74	2.0E-03	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5013	10116	15248	1	2.0E-03	D38157.1	NT	Equine rotavirus RNA 5 for NSP1, complete cds, strain: H2
5013	10116	15249	1	2.0E-03	D38157.1	NT	Equine rotavirus RNA 5 for NSP1, complete cds, strain: H2



Page 59 of 214  
Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
438	5607	10751	1.94	1.0E-03	H98471.1	EST_HUMAN	y98008.r1 Soares_pineal_gland_NH-IPG Homo sapiens cDNA clone IMAGE:232334 5'
830	5982	11150	1.37	1.0E-03	A1720283.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE ;
830	5982	11151	1.37	1.0E-03	A1720283.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE ;
1096	6234	11397	3.44	1.0E-03	A1865788.1	EST_HUMAN	wk56a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422288 3'
1116	6254	11418	2.36	1.0E-03	A1954572.1	EST_HUMAN	wc93e10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
1168	6303	11469	1.32	1.0E-03	A1692616.1	EST_HUMAN	wd86a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
2021	7139	12378	2.71	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMWI)
2137	7251	12497	1.97	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
2850	8104	13269	1.23	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3174	8325	13486	2.13	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3174	8325	13487	2.13	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3284	8433	13595	0.8	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3530	8672	13837	0.8	1.0E-03	U68081.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3530	8672	13838	0.8	1.0E-03	U68081.1	NT	Human MUC2 gene, promoter region
3642	8781		1.48	1.0E-03	AB044400.1	NT	Human MUC2 gene, promoter region
3898	9034	14193	1.14	1.0E-03	AW170562.1	EST_HUMAN	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
3907	9043	14203	0.65	1.0E-03	Z49848.1	NT	xn63d07.x1 Soares_NH/CeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698381 3' similar to contains TAR1.11 TAR1 repetitive element ;
4412	9532	14671	2.51	1.0E-03	BE939162.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR149w
4455	9574	14713	3.89	1.0E-03	BE246536.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4633	9751	14898	0.8	1.0E-03	U29449.1	NT	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4792	9905	15045	2.14	1.0E-03	A073485.1	EST_HUMAN	Ceenorhabdilis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4792	9905	15046	2.14	1.0E-03	A073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4793	9906		5.88	1.0E-03	BET54087.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
5080	10182	15295	10.91	1.0E-03	O46409	SWISSPROT	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5196	10293	15430	2.15	1.0E-03	AW297269.1	EST_HUMAN	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
1498	6625		1.19	8.0E-04	X96469.1	NT	JI-H-BW0-ajl-d-08-Q-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731838 3'
4151	9277		5.04	8.0E-04	P08547	SWISSPROT	X.laeviis mRNA for CAsR protein
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4730	9843	14989	2.53	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1841	6962	12185	1.06	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2376	7492	12736	1.02	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2675	7772	13023	3.11	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3264	8413	13575	0.97	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3931	9067	14223	1.49	6.0E-04	A1862525.1	EST_HUMAN	w15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4156	9282	14418	3.13	6.0E-04	U45983.1	NT	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds
4421	9541	14680	0.9	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-09 HT0560 Homo sapiens cDNA
4421	9541	14681	0.9	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-09 HT0560 Homo sapiens cDNA
5003	10108		1.07	6.0E-04	L40808.1	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5180	10277	15415	1.88	6.0E-04	BE089220.1	EST_HUMAN	CM2-BT0698-230300-128-10 BT0698 Homo sapiens cDNA
650	5811	10946	9.89	5.0E-04	O10341	SWISSPROT	HYPOPHOSPHATASE 2, 3 KD PROTEIN (ORF92)
1516	6643		1.17	6.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-07 CT0225 Homo sapiens cDNA
3395	8539	13698	1.31	5.0E-04	AA549931.1	EST_HUMAN	nk27e11.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014784 3' similar to contains Alu repetitive element
390	5559		0.64	4.0E-04	BF241482.1	EST_HUMAN	601876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
672	5831	10971	1.09	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
848	5999	11170	1.25	4.0E-04	A1720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825
848	5999	11171	1.25	4.0E-04	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
1477	6604	11790	2.44	4.0E-04	AW753353.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825
2076	7192	12436	1.04	4.0E-04	AL163278.2	NT	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
2582	7693	12947	1.2	4.0E-04	O56615	SWISSPROT	RC3-CT0284-130100-023-01 CT0284 Homo sapiens cDNA
3143	8294	13492	3.12	4.0E-04	AF281074.1	NT	Homo sapiens chromosome 21 segment HS21C078
4300	9422	14554	3.09	4.0E-04	AA576331.1	EST_HUMAN	SERPIN-2 (SILK GUM PROTEIN 2)
4300	9422	14555	3.09	4.0E-04	AA576331.1	EST_HUMAN	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4510	9626	14773	2.08	4.0E-04	AA098324.1	EST_HUMAN	nt10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb.M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5072	10173	15308	3.37	4.0E-04	BE560660.1	EST_HUMAN	nt10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb.M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5184	10281	15419	1.76	4.0E-04	Q06846	SWISSPROT	zn161c08.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'
151	5348	10490	1.81	3.0E-04	AL119426.1	EST_HUMAN	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
192	5387	10530	1.92	3.0E-04	P49259	SWISSPROT	RABPHILIN-3A
							DKFZp761J221.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
							180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
881	6031	11203	1.8	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1852	6873	12194	1.38	3.0E-04	AI262100.1	EST_HUMAN	q228d03.y1 NCJ_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2028197 5'
1855	6955		2.63	3.0E-04	AI399574.1	EST_HUMAN	th23a02.x1 NCJ_CGAP_P728 Homo sapiens cDNA clone IMAGE:2116082 3'
3290	8438	13599	3.58	3.0E-04	P25147	SWISSPROT	INTERALIN B PRECURSOR
3936	9072	14228	4.2	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4030	9161		1.23	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4069	9199		1.08	3.0E-04	BE140609.1	EST_HUMAN	RCO-HT0014-310589-028 HT0014 Homo sapiens cDNA
4785	9898		4.72	3.0E-04	BE153778.1	EST_HUMAN	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
171	5368	10507	1.36	2.0E-04	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
478	5845	10786	2.85	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
908	6058	11227	8.82	2.0E-04	M86524.1	NT	Human dystrophin gene
908	6058	11228	8.82	2.0E-04	M86524.1	NT	Human dystrophin gene
1181	6316		4.31	2.0E-04	AI286021.1	EST_HUMAN	q198e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
1188	6322		4.78	2.0E-04	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1846	6967		0.99	2.0E-04	AF224288.1	NT	Mus musculus 5' flanking region of Pib3 gene
2166	7279		0.99	2.0E-04	AA478980.1	EST_HUMAN	z139b05.s1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2639	7642	12891	2.8	2.0E-04	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBV1S1, TCRBV1S2, >
2956	8110	13273	0.83	2.0E-04	AI124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3318	8463	13626	0.68	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3417	8560	13717	2.45	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0386-070500-194-b07 BT0386 Homo sapiens cDNA
3888	9024	14182	0.87	2.0E-04	AW978441.1	EST_HUMAN	EST390550 MAGP resequences, MAGP Homo sapiens cDNA
4114	9242		6.91	2.0E-04	U01029.1	NT	Phasolus vulgaris nitrate reductase (PVNRR2) gene, complete cds
4639	9757	14904	1.35	2.0E-04	H66265.1	EST_HUMAN	y01e11.1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4639	9757	14905	1.35	2.0E-04	H66265.1	EST_HUMAN	y01e11.1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4764	9877		1.65	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5040	10142	15272	1.69	2.0E-04	AB037997.1	NT	Danio rerio hagoromo gene, exons 1 to 6, partial cds
787	5921	11078	1.21	1.0E-04	H99646.1	EST_HUMAN	y26c09.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:262884 3' similar to contains L1.1 L1 repetitive element;

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1076	6216	11380	2.02	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
1115	6253	11416	3.41	1.0E-04	AW013947.1	EST_HUMAN	U1-H-B10-aab-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1115	6253	11417	3.41	1.0E-04	AW013947.1	EST_HUMAN	U1-H-B10-aab-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1337	6455		3.38	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
							Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1638	6767	11950	2.62	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1638	6767	11951	2.62	1.0E-04	AF148805.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
1872	6802	12217	1.68	1.0E-04	AB048342.1	NT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPICING FACTOR 3A SUBUNIT 2) (SF3A66)
3268	8417	13579	0.97	1.0E-04	Q62203	SWISSPROT	U01111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element
3717	8555	14009	0.71	1.0E-04	AI440282.1	EST_HUMAN	Mouse alpha 1 type-IV collagen mRNA
4034	9165	14307	2.12	1.0E-04	MT4042.1	NT	AV647727 GLC Homo sapiens cDNA clone GLCBB04 3'
4059	9180	14331	1.38	1.0E-04	AV647727.1	EST_HUMAN	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5080	10181	16317	1.46	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5080	10181	16318	1.48	1.0E-04	7662015	NT	U1-H-B10-aab-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2005975 3'
5084	10184	15322	0.92	1.0E-04	AI357156.1	EST_HUMAN	U1-H-B10-aab-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2796928 3'
5202	10299	15436	0.97	1.0E-04	AW451457.1	EST_HUMAN	U1-H-B10-aab-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2796928 3'
6068	5653	10998	2.38	9.0E-05	AA718933.1	EST_HUMAN	U1-H-B10-aab-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2796928 3'
822	5975	11139	1.19	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
865	6016		7.43	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
2916	8070		0.77	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4460	9579	14716	0.71	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Sceres NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
5201	10298	15435	0.96	8.0E-05	L36918.1	NT	Pig microsatellite DNA (CA repeat)
344	5527	10663	7.12	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
344	5527	10664	7.12	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
506	5731	10659	1.01	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human foovea cDNA Homo sapiens cDNA clone EST HFD072014
506	5731	10660	1.01	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human foovea cDNA Homo sapiens cDNA clone EST HFD072014
							PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
1057	6168	11363	1.65	7.0E-05	Q22949	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
2680	7777	13027	2.29	7.0E-05	AL163278.2	NT	

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3137	8288	13445	5.82	7.0E-05	AB009080.1	NT	Dichytellium discoidale gene for TRFA, complete cds
4351	9473	14811	1.64	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2020	7137	12376	1.27	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2020	7137	12377	1.27	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2550	7653	12903	1.14	6.0E-05	AI655241.1	EST_HUMAN	W554106.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA TOPOISOMERASE 1 (HUMAN);
2775	5836	10975	2.57	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
1411	6538	11715	35.84	5.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241199-040-H11 ST0234 Homo sapiens cDNA
1874	6994		1.42	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
3952	9087	14241	3.47	5.0E-05	AJ251864.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
2768	6419		3.52	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
4461	9550	14717	0.53	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4461	9550	14718	0.53	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4846	9938		1.17	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
5004	10109	15238	0.62	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
679	5837	10977	0.84	3.0E-05	AJ248061.1	EST_HUMAN	q164c10.x1 Soares_fetal_liver_spleen_INFILS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element contains element KER repetitive element ;
1050	6201	11365	1.2	3.0E-05	AW273951.1	EST_HUMAN	xv24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1132	6269	11431	1.4	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
1132	6269	11432	1.4	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
2682	7779	13029	1.13	3.0E-05	Q62234	SWISSPROT	SKELEMIN
4361	9483	14623	5.06	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4361	9483	14624	5.06	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4445	9564	14705	1.08	3.0E-05	AA368679.1	EST_HUMAN	EST79996 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4445	9564	14706	1.08	3.0E-05	AA368679.1	EST_HUMAN	EST79996 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4704	9820	14967	1.03	3.0E-05	P97468	SWISSPROT	CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ)
4804	5837	10977	0.62	3.0E-05	AJ248061.1	EST_HUMAN	q164c10.x1 Soares_fetal_liver_spleen_INFILS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element contains element KER repetitive element ;
4811	9923	15084	0.98	3.0E-05	AU125721.1	EST_HUMAN	AU125721 NT2RM4 Homo sapiens cDNA clone NT2RM4002075 5'
2304	7413	12663	1.03	2.0E-05	AJ286021.1	EST_HUMAN	q168e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2547	7650	12899	1.02	2.0E-05	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
2874	7771		3.85	2.0E-05	AA160562.1	EST_HUMAN	zq46a12.11 Striatogene HNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element contains element L1 repetitive element ;

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3115	8288	13424	1.29	2.0E-05	BE06036.1	EST_HUMAN	RC3-BT0319-120200-014-H08 BT0319 Homo sapiens cDNA
3330	8476	13639	0.66	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3351	8496	13665	0.94	2.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
3475	8617		0.62	2.0E-05	X95465.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
4584	9702	14841	0.63	2.0E-05	A1283349.1	EST_HUMAN	qg13a08.x1 Soares_Nh-MP_u_S1 Homo sapiens cDNA clone IMAGE:1932374 3' similar to contains
5010	10113		1.08	2.0E-05	L77569.1	NT	MER18.b3 MER18 repetitive element ;
2656	7948	13002	1.15	1.0E-05	AL163282.2	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
3627	8766	13922	1.94	1.0E-05	AF088279.1	NT	Homo sapiens chromosome 21 segment HS21C082
3790	8927		0.99	1.0E-05	AF223391.1	NT	Drosophila melanogaster strain Lanto 120 Suppressor of Hairless (Su(H)) gene, partial cds
3940	9076	14230	0.21	1.0E-05	P81274	SWISSPROT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4144	9272	14409	1.2	1.0E-06	AL163203.2	NT	MOSAIC PROTEIN LGN
4251	9376	14507	1.94	1.0E-05	AA431119.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
4820	9932	15073	1.81	1.0E-05	AW419134.1	EST_HUMAN	zw69g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4954	10062	15201	0.7	1.0E-05	Z18943.1	NT	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856948 3'
2633	7731	12998	2.62	9.0E-06	A1563811.1	EST_HUMAN	H. sapiens repeat region
3069	8222	13373	4.49	9.0E-06	A1218983.1	EST_HUMAN	tt73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3594	8733		3.18	9.0E-06	M61755.1	NT	qg11b08.x1 Soares_placenta_8tc9weeks_2Nb-HP8tc9w Homo sapiens cDNA clone IMAGE:1759191 3'
2501	7941	12853	3.36	8.0E-06	AW362839.1	EST_HUMAN	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
990	6126		1.45	7.0E-06	AA669729.1	EST_HUMAN	RC3-CT0283-201189-011-h11 CT0283 Homo sapiens cDNA
1449	6577	11784	3.8	7.0E-06	7662177	NT	ab00710.s1 Striatagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains
2837	7992		6.1	7.0E-06	A1368252.1	EST_HUMAN	MER20.t1 MER20 repetitive element ;
3549	8690		1.44	7.0E-06	AA385542.1	EST_HUMAN	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2883	8037	13202	1	6.0E-06	BE069189.1	EST_HUMAN	qwt6g09.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991266 3' similar to contains Alu repetitive element;
3669	8808	13965	1.08	6.0E-06	BE069189.1	EST_HUMAN	EST769205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
4716	8061	13232	1.93	6.0E-06	Q01456	SWISSPROT	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4726	9839	14983	2.52	6.0E-06	A1040089.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
646	5807	10941	6.07	4.0E-06	R16267.1	EST_HUMAN	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
							alpha08a02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656738 3' similar to contains MER8.12 MER8 repetitive element ;
							ya48c03.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element ;

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
847	5998	11169	5.54	4.0E-06	AW103354.1	EST_HUMAN	xc59g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element;
1339	6467	11647	2.81	4.0E-06	A1334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1339	6467	11648	2.81	4.0E-06	A1334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1485	6612	11799	1.68	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200800-250-J07 NT0048 Homo sapiens cDNA
2245	7356	12613	1.14	4.0E-06	AW015401.1	EST_HUMAN	U1-H-B10-eat-f05-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3038	8190	13348	0.74	4.0E-06	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3871	9007	14163	1.07	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4778	9889	15034	2.18	4.0E-06	A186939.1	EST_HUMAN	W194c10.x1 NCI_CGAP_Bnc25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element;
2145	7259	12505	0.96	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432683 3' similar to contains L1.11 L1 repetitive element;
2145	7259	12506	0.96	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432683 3' similar to contains L1.11 L1 repetitive element;
2247	7357		1.18	3.0E-06	AF202835.1	NT	Homo sapiens PP1200 mRNA, complete cds
2887	8041	13205	0.94	3.0E-06	AA668218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element;
3248	8398		2.34	3.0E-06	A1857779.1	EST_HUMAN	w122a05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN ; contains L1.12 L1 repetitive element ;
3762	8899	14050	1.42	3.0E-06	BE047094.1	EST_HUMAN	hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3762	8899	14051	1.42	3.0E-06	BE047094.1	EST_HUMAN	hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4454	9573	14712	0.86	3.0E-06	T50266.1	EST_HUMAN	y678b10.r1 Stratiogene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4535	9653	14798	3.81	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
199	5394		2.1	2.0E-06	P54368	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1582	8711		4.44	2.0E-06	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
2357	7464	12720	2.79	2.0E-06	A1872138.1	EST_HUMAN	w604a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297088 3' similar to contains MER30.b1 repetitive element ;
2443	7547	12800	1.72	2.0E-06	P04029	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2534	7637	12885	1.17	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3504	8845	13811	1.05	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB06 3'
3742	8980	14031	1.74	2.0E-06	AA173518.1	EST_HUMAN	zp02e05.r1 Stratiogene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3753	8990	14041	0.63	2.0E-06	AW450215.1	EST_HUMAN	U1-H-B13-aky-g-05-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3757	8894	14044	1.44	2.0E-08	AB030898.1	NT	Mus musculus gene for odorant receptor A16, complete cds
32	5243	10359	2.94	1.0E-06	O76082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
656	5817	10955	1.39	1.0E-06	AF084364.1	NT	Mus musculus D6M5E protein (D6M5e) mRNA, complete cds
1464	6591	11779	1.35	1.0E-06	P09125	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
1585	6714	11904	1.22	1.0E-06	AA034141.1	EST_HUMAN	z08a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to contains Alu repetitive element;
1585	6714	11905	1.22	1.0E-06	AA034141.1	EST_HUMAN	z08a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to contains Alu repetitive element;
1597	6726		1.1	1.0E-06	P27826	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
1995	7112	12346	3.66	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1995	7112	12347	3.66	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4348	9470	14607	12.32	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5088	10188	15327	1.04	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5088	10188	15328	1.04	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
358	5539	10680	1.19	9.0E-07	AF003529.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
358	5539	10681	1.19	9.0E-07	AF003529.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
4736	9849	14995	4.45	8.0E-07	AI288596.1	EST_HUMAN	q182g07.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4736	9849	14996	4.45	8.0E-07	AI288596.1	EST_HUMAN	q182g07.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
1915	7034	12254	2.17	6.0E-07	AW855558.1	EST_HUMAN	CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
2485	7569	12823	2.3	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
3945	9081		1.72	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4.P33 INTERGENIC REGION
324	5509		1.21	5.0E-07	AB31893.1	EST_HUMAN	WB4410.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1059	6200		3.61	5.0E-07	A4380630.1	EST_HUMAN	EST193615 Supt cells Homo sapiens cDNA 5' end
3003	8157		0.61	5.0E-07	AB31893.1	EST_HUMAN	WB4410.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4615	9733	14870	0.98	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
3974	9108	14257	1.94	4.0E-07	AW006602.1	EST_HUMAN	ws84h05.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504697 3'
440	5609	10763	3.66	3.0E-07	U19719.1	NT	Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
581	5744	10872	3.16	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1383	6511	11692	1.46	3.0E-07	M69149.1	NT	Human polymorphic microsatellite DNA



Page 67 of 214  
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1637	6768		1.48	3.0E-07	M64857.1	NT	Human IgK subgroup J germline gene, exons 1 and 2, V-region 018 allele.
2446	7546	12802	19.22	3.0E-07	BE005077.1	EST_HUMAN	MRO-BND115-020300-001-f11 BND115 Homo sapiens cDNA
2445	7549	12803	19.22	3.0E-07	BE005077.1	EST_HUMAN	MRO-BND115-020300-001-f11 BND115 Homo sapiens cDNA
3008	8160	13317	0.87	3.0E-07	T84704.1	EST_HUMAN	Y450F12.1 Soares fetal liver spleen INFL3 Homo sapiens cDNA IMAGE:111695 5'
3138	8289	13446	1.67	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4895	9811	14959	7.36	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCDD01 3'
4728	9841	14986	0.72	3.0E-07	AF797236.1	EST_HUMAN	we85b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347967 3'
5046	10148	15277	1.3	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5048	10148	15278	1.3	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
27	5238	10353	2.63	2.0E-07	AF282988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
149	6346	10488	10.59	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
149	5346	10489	10.59	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
177	5371	10512	133.71	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic (vascular) actin gene, complete cds
747	5903	11057	1.67	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
747	5903	11058	1.67	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
759	5914		1.19	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
943	6091	11259	2.03	2.0E-07	AA223260.1	EST_HUMAN	z08b07.s1 Stralagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:U18800 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
944	6092	11260	4.38	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element ;
1165	6300	11466	0.92	2.0E-07	Q26768	SWISSPROT	U6 AUTOANTIGEN
1614	6742	11937	2.37	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3665	8804	13960	17.65	2.0E-07	AF126348.1	NT	Homo sapiens ceveolin 1 (CAV1) gene, exon 3 and partial cds
1103	8241		0.89	1.0E-07	AL163232.2	NT	Homo sapiens chromosome 21 segment HS21C082
2787	6665	11851	2.67	1.0E-07	P09266	SWISSPROT	GLYCOPROTEIN GPV
3726	6241		0.93	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4269	9393	14531	2.63	1.0E-07	AV118662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4269	9393	14532	2.63	1.0E-07	AV118662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4708	9824		1.46	1.0E-07	O75820	SWISSPROT	ZINC FINGER PROTEIN 189
604	7895		2.32	8.0E-08	AI911352.1	EST_HUMAN	wd16605.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1052	6193		0.77	8.0E-08	BE795489.1	EST_HUMAN	601590:133F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3943976 5'
3532	8674		1.6	8.0E-08	BE795489.1	EST_HUMAN	601590:133F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3943976 5'
77	5286	10428	2.93	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1370	6498	11881	30.42	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3563	8704	13864	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3563	8704	13865	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
818	5971	11132	2.76	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
818	5971	11133	2.76	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2343	7450	12705	2.87	6.0E-08	BE144398.1	EST_HUMAN	MRO-1T0166-191169-004-g09 HT0166 Homo sapiens cDNA
3034	8188	13344	0.85	6.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4226	9351	14484	1.03	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
81	5290	10430	2.3	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2217	7329	12582	1.58	5.0E-08	AA493851.1	EST_HUMAN	nh03b09.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
1771	6897	12103	1.14	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1771	6897	12104	1.14	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2852	8007		1	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0426_r1 434 (synonym: hesc3) Homo sapiens cDNA clone DKFZp434J0426 5'
203	5398		11.08	2.0E-08	AW302968.1	EST_HUMAN	x87106.x1 NCL_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2787139 3'
226	5420		5.39	2.0E-08	AA425598.1	EST_HUMAN	zw4807.r1 Soares_t01a_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element;
496	5663	10799	8.75	2.0E-08	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
659	5820	10957	9.78	2.0E-08	AW886438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
659	5820	10958	9.78	2.0E-08	AW886438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
991	6138		32.06	2.0E-08	BE280477.1	EST_HUMAN	801155321F1 NIH_MGC.21 Homo sapiens cDNA clone IMAGE:3138893 5'
1348	6477	11657	2.11	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1752	6878		1.38	2.0E-08	BE734871.1	EST_HUMAN	801570463F1 NIH_MGC.21 Homo sapiens cDNA clone IMAGE:3846189 5'
1866	6988		3.06	2.0E-08	AW270271.1	EST_HUMAN	xp43f11.x1 NCL_CGAP_JHN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2514	7618		1.97	2.0E-08	K00216.1	NT	Sheep His-JRNA-GUG
3192	8343	13506	5.72	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3192	8343	13507	5.72	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3838	8974		1.96	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-b03 ST0197 Homo sapiens cDNA
4053	9184	14326	0.65	2.0E-08	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4384	9505		2.53	2.0E-08	AA458040.1	EST_HUMAN	aa26c07.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element;

Page 69 of 214  
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4937	10047		2.73	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element;
1653	6781	11973	4.03	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)
1653	6781	11974	4.03	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)
1765	6911	12119	1.06	1.0E-08	AF126348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
2043	7159		1.82	1.0E-08	BE141959.1	EST_HUMAN	PM2-HT0130-150999-001-112 HT0130 Homo sapiens cDNA
3176	8326	13488	0.95	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3175	8326	13489	0.95	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
4221	9346	14478	4.46	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
4221	9346	14479	4.46	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3592	8731		1.83	7.0E-09	D86842.1	NT	Homo sapiens DNA for 3-kelocacyl-Oa thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
3983	9117		0.96	7.0E-09	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
4955	10073	15211	5.03	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-150200-001-105 HT0527 Homo sapiens cDNA
1423	6550	11731	2.7	5.0E-09	BE149264.1	EST_HUMAN	RC2-HT0262-120200-014-110 HT0262 Homo sapiens cDNA
1864	6994	12208	1.01	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5163	10261	15399	0.72	5.0E-09	AW605894.1	EST_HUMAN	RC4-HT0251-140100-013-g08 HT0251 Homo sapiens cDNA
5183	10261	15400	0.72	5.0E-09	AW605894.1	EST_HUMAN	RC4-HT0251-140100-013-g08 HT0251 Homo sapiens cDNA
519	5685		1.52	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
966	6113		2.36	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1481	6608	11794	3	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2407	7513	12763	23.69	4.0E-09	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' and similar to similar to heat shock protein, 90 kDa
2331	7498	12691	2.77	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.3
3148	8299	13459	3.93	3.0E-09	AW296435.1	EST_HUMAN	MER18 repetitive element;
3310	8457	13619	0.94	3.0E-09	BE222239.1	EST_HUMAN	UL-H.BW0-ak-a-08-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730134 3'
3358	8503		0.61	3.0E-09	AA442272.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.3
4072	9202		0.6	3.0E-09	X16674.1	NT	MER18 repetitive element;
4404	9524	14665	3.68	3.0E-09	AF176325.1	NT	z654a04.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
							H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
							Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds

Page 70 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4486	9805	14743	1.47	3.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
4754	9867	15016	0.96	3.0E-09	AW473832.1	EST_HUMAN	xy17h02.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2863459 3' similar to SW:ELF1_DROME
813	5988		0.84	2.0E-09	X10874.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1262	6391	11567	4.89	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1671	6800		7.76	2.0E-09	AL118573.1	EST_HUMAN	DKFZp781B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781B1710 5'
2307	7416	12686	8.31	2.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
3910	8046	14205	3.18	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
1110	6248	11411	2.27	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1110	6248	11412	2.27	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1644	6772		0.95	1.0E-09	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2866	8011	13173	1.65	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2891	8045	13209	6.75	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2891	8045	13210	5.75	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3010	8164	13321	0.87	1.0E-09	BE636440.1	EST_HUMAN	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4767	9880		5.33	1.0E-09	AA719297.1	EST_HUMAN	z135b03.s1 Soares, pineal gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
5182	10202	15341	10.98	1.0E-09	T60216.1	EST_HUMAN	yc22c09.r1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:81424 5' similar to contains Alu repetitive element; contains MER28 repetitive element;
1313	6443	11620	1.33	9.0E-10	AW867740.1	EST_HUMAN	MR0-SN0040-050300-002-c07 SN0040 Homo sapiens cDNA
2795	7952	13118	5.85	9.0E-10	A1870071.1	EST_HUMAN	we78h03.x1 Soares, Dialectraefe colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 contains element PTR5 repetitive element;
142	5339	10483	8.8	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3324	8471	13633	0.83	8.0E-10	BE080748.1	EST_HUMAN	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
4173	9299	14434	3.5	8.0E-10	A4379632.1	EST_HUMAN	EST189564 Small intestine I Homo sapiens cDNA 5' end
699	5856	11003	33.6	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
699	5856	11004	33.6	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1634	6763	11958	1.86	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2528	7631		5.19	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3080	8213	13366	2.31	7.0E-10	X00856.1	NT	H.sapiens DHFR gene, exon 3
914	6084	11230	4.11	8.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2639	7737	12990	1.07	6.0E-10	AI424405.1	EST_HUMAN	h02407.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2095021 3'
4707	9823		2.83	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031099-012-g12 CT0254 Homo sapiens cDNA
760	5915		4.22	5.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N219 5'
3457	8589	13763	1.18	5.0E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
4976	10084	15219	1.16	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
107	5311		2.24	4.0E-10	A1221083.1	EST_HUMAN	qg09f09.x1 Soares_placenta_8to9weeks_2Nb-HP8c9W Homo sapiens cDNA clone IMAGE:1759049 3'
579	5742	10870	1.14	4.0E-10	AA515260.1	EST_HUMAN	similar to contains LTR8.b2.LTR8 repetitive element;
1897	7114	12349	1.78	4.0E-10	AW594709.1	EST_HUMAN	h64a01.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:924648 3'
2538	7641	12890	2.55	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
916	6065	11232	1.24	3.0E-10	N36113.1	EST_HUMAN	Y62f06.s1 Soares_melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272983 3' similar to contains L1 L1 repetitive element;
1358	6487		4.99	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
34	5245	10361	1.66	2.0E-10	P49988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
34	5245	10362	1.68	2.0E-10	P49988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1904	7023		2.47	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2955	8109		0.93	2.0E-10	BF675047.1	EST_HUMAN	502136640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
1620	6748	11942	2.68	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXA11 3'
2546	7649		2.2	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-191199-058-e08 CT0225 Homo sapiens cDNA
3482	8623	13790	1.85	1.0E-10	AW632912.1	EST_HUMAN	QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA
3527	8669		1.24	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3821	8669		1.14	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3990	9124		4.98	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4099	9228	14364	5.13	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
4099	9228	14365	5.13	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
4105	9234	14372	1.92	1.0E-10	AB031069.1	NT	Homo sapiens PCOX1 mRNA for protein containing CXXC domain 1, complete cds
4141	9259		2	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon

Page 72 of 214  
Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
269	5449	10588	0.92	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-291099-018-c08 HT0203 Homo sapiens cDNA
2095	7210	12456	3.33	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
2096	7210	12457	3.33	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
3364	8509	13677	2.63	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
3364	8509	13678	2.63	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
4949	10058	15196	1.24	9.0E-11	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3092	8245		7.83	8.0E-11	H19971.1	EST_HUMAN	Yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element
4017	9150	14292	4.86	8.0E-11	N23712.1	EST_HUMAN	yw46e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
1460	6587	11775	1.36	7.0E-11	AA330942.1	EST_HUMAN	EST34392 Embryo, 6 week 1 Homo sapiens cDNA 5' end
411	5579	10728	5.87	8.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
411	5579	10729	5.87	8.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
11	5222	10334	0.97	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3346	5222	10334	1.36	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4206	9331	14464	1.3	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
5189	10286	15422	0.95	5.0E-11	D43770.1	NT	Homo sapiens RNA for differentiation of sex determination
1408	6535		1.15	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:730559 5'
2761	7845	13100	4.78	4.0E-11	BE885900.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909285 5'
2939	8083	13260	0.98	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4589	9707	14846	0.88	4.0E-11	D44666.1	EST_HUMAN	HUMSUPY089 Human brain cDNA Homo sapiens cDNA clone 089
1502	6629	11816	9.87	3.0E-11	6878077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
4250	9375		1.22	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
981	6109	11278	1.33	2.0E-11	A1150502.1	EST_HUMAN	q336c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1187	6321	11490	3.67	2.0E-11	R24807.1	EST_HUMAN	MER10 repetitive element
1187	6321	11491	3.67	2.0E-11	R24807.1	EST_HUMAN	y93e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1626	6754	11947	3.35	2.0E-11	L17432.1	NT	y93e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1626	6754	11948	3.35	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, epsilon-globin, and olfactory receptor-like protein
2726	7821	13076	1.04	2.0E-11	AF087913.1	NT	COR3 beta (COR3 beta) genes, complete cds
3179	8330	13494	6.54	2.0E-11	P10263	SWISSPROT	Gallus gallus rho-globin, beta-H globin, epsilon-globin, and olfactory receptor-like protein
3307	8454	13616	0.77	2.0E-11	A1478617.1	EST_HUMAN	Human endogenous retrovirus HERV-P-747D
4422	9542		1.16	2.0E-11	BE065637.1	EST_HUMAN	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
							Im54c09.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161836 3'
							RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA

Page 73 of 214  
Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4579	9897		0.85	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
4912	10022		2.2	2.0E-11	BE062558.1	EST_HUMAN	QV2-B10258-261098-014-e01 BT0258 Homo sapiens cDNA
4992	10098	16228	0.91	2.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
5014	10117	15250	0.62	2.0E-11	AA307331.1	EST_HUMAN	EST178228 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to alpha-2-macroglobulin
676	5833	10973	0.63	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
784	5939	11097	1.43	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1220	6352	11521	2.28	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1513	6640		1.47	1.0E-11	AF118914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2031	7149	12388	1.31	1.0E-11	P16268	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2118	7233	12475	1.5	1.0E-11	AF00573.1	NT	Homo sapiens homotetrasite 1,2-dioxygenase gene, complete cds
3480	8621	13786	0.71	1.0E-11	BE004315.1	EST_HUMAN	GM0-BN0105-170300-262-412 BN0105 Homo sapiens cDNA
2918	8072	13242	0.8	9.0E-12	P26742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
4631	9749	14895	1.49	7.0E-12	Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
3534	8976		0.83	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAW F06 5'
4325	9447	14580	9.03	6.0E-12	AA732516.1	EST_HUMAN	nz88f11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
1045	6186	11353	2.75	5.0E-12	T06573.1	EST_HUMAN	EST04482 Fetal brain, Stragelene (cat#836208) Homo sapiens cDNA clone HFB0V33
3371	8516	13683	1.09	5.0E-12	BE047779.1	EST_HUMAN	tz42b05.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291217 5'
3709	8846	14000	6.31	5.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
241	5433	10572	3.41	4.0E-12	AA700328.1	EST_HUMAN	zj74g11.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
242	5433	10572	3.58	4.0E-12	AA700326.1	EST_HUMAN	zj74g11.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4590	9708	14846	0.72	4.0E-12	AI689984.1	EST_HUMAN	b26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13639 Q13539
613	5773	10903	3.9	3.0E-12	AW341883.1	EST_HUMAN	MARINER TRANSPOSASE ; hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517
613	5773	10904	3.9	3.0E-12	AW341883.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517
1666	6794	11889	1.46	2.0E-12	AW802131.1	EST_HUMAN	O14517 SMRP ; IL5-UM0071-120400-065-a05 UM0071 Homo sapiens cDNA
3448	8590	13754	0.87	2.0E-12	6754495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4090	9218	14364	2.24	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4090	9218	14355	2.24	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4399	9519		2.08	2.0E-12	BE063509.1	EST_HUMAN	CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA

Page 74 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
118	5319	10462	1.53	1.0E-12	AW627674.1	EST_HUMAN	hh90a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11 MER18 repetitive element ;
1988	7105		1.25	1.0E-12	AJ871726.1	EST_HUMAN	wm51f07.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element ;
3042	8196	13351	0.92	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3042	8196	13352	0.92	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3852	8988	14143	27.54	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3852	8988	14144	27.54	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3918	9054	14215	0.9	9.0E-13	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
715	5872	11019	4.71	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
715	5872	11020	4.71	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1851	6972	12193	2.14	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2092	7207	12453	6.92	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3303	8450		0.61	5.0E-13	R76398.1	EST_HUMAN	y82f04.r1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:145759 5'
3378	8523		1.24	6.0E-13	AA435773.1	EST_HUMAN	z77a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
1878	8998		8.88	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA
2437	7541		1.18	4.0E-13	AF003629.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
175	5389		3.86	3.0E-13	AF003628.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
866	6017		4.09	3.0E-13	AA430310.1	EST_HUMAN	zw88g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
2350	7457	12712	0.96	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2452	7556		1.57	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2625	7724	12977	2.84	3.0E-13	BF372962.1	EST_HUMAN	CM3-FT0100-140700-242-H08 FT0100 Homo sapiens cDNA
3189	8320		2.2	3.0E-13	AA145844.1	EST_HUMAN	ob18d02.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
145	5342	10486	2.57	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adenosine diphosphate protein >
236	5429	10569	0.95	2.0E-13	U23899.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cde
1274	6403	11577	13.57	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3255	8414	13576	1.13	2.0E-13	BF431899.1	EST_HUMAN	nab78f05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'



Page 75 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3491	8632	13799	1.19	2.0E-13	AF106907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4084	9213		1.65	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
289	5477	10618	1.12	1.0E-13	S74129.1	NT	FGF-1-fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
889	6039	11210	3.99	1.0E-13	AJ007873.1	NT	Homo sapiens LGMD2B gene
1341	6469	11650	1.23	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, PP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2017	7134	12372	8.56	1.0E-13	AA720574.1	EST_HUMAN	mw21g02.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
4565	9683	14822	1.57	1.0E-13	BF340987.1	EST_HUMAN	602038009F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185966 5'
331	5514	10651	3.32	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.H MER19 repetitive element;
332	5515	10652	2.67	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.H MER19 repetitive element;
2471	7575		1.95	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2553	7656	12907	0.99	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2553	7656	12908	0.99	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2717	7812	13067	3.37	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3087	8240	13389	4.51	9.0E-14	AW513286.1	EST_HUMAN	xc54h05.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707833 3'
3223	5514	10651	0.72	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.H MER19 repetitive element;
3775	8912	14065	6.58	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4722	9836	14980	1.8	9.0E-14	AJ002153.1	NT	Saginus oedipus gene for seminal vesicle secreted protein semenogelin I
3478	8619		1.27	8.0E-14	BE468263.1	EST_HUMAN	hz71c09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
3928	9084		3.4	8.0E-14	R76269.1	EST_HUMAN	yt72e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144798 3'
1639	7922		3.39	7.0E-14	AW151673.1	EST_HUMAN	x67e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.12 MER10 repetitive element;
365	5545	10687	11.15	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
615	5775	10906	4.88	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5035	10137	15270	1.36	5.0E-14	AW073791.1	EST_HUMAN	xc03b05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1 repetitive element;
1124	7909		1.65	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR

Page 76 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1888	7008	12228	4.53	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3733	8871		0.65	4.0E-14	AA046502.1	EST_HUMAN	zkg7a06.r1 Soares_pregnanter_uterus_NbIFU Homo sapiens cDNA clone IMAGE:487858 5'
4268	9392	14530	0.95	4.0E-14	N46328.1	EST_HUMAN	W73c12.s1 Soares_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element;
951	6099	11267	1.16	3.0E-14	X95453.1	NT	R.norvegicus mRNA for CPG2 protein
4905	10015	15159	0.65	3.0E-14	AW265354.1	EST_HUMAN	xp45f1.2.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MERG repetitive element;
388	5557	10701	2.38	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
388	5557	10702	2.38	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
688	7897	10987	9.97	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2365	7471		1.07	2.0E-14	AW372868.1	EST_HUMAN	RC5-BT0377-091298-031-D12 BT0377 Homo sapiens cDNA
2441	7545		0.98	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2636	7734		2.48	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1068	6208	11371	2.48	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1414	6541	11718	6.76	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1414	6541	11719	5.76	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2002	7119	12355	22.17	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2187	7280	12526	2.46	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2386	7492	12745	23.6	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2910	8064	13236	1.11	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-I)
3146	8297	13456	5.64	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3146	8297	13457	5.64	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3863	8989	14156	1.84	1.0E-14	AA682694.1	EST_HUMAN	ae89c12 st Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:2753059 3'
4452	9571	14710	1.81	1.0E-14	AW275852.1	EST_HUMAN	xg39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
1589	6718	11907	1.49	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2772	5847		1.52	8.0E-15	BE261482.1	EST_HUMAN	601148632FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
995	6141	11310	7.37	6.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
409	5577	10725	5.25	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3450	8592		1.01	5.0E-15	AW296817.1	EST_HUMAN	UI-HBW0-ajb-g-10-0-LJI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2731219 3'
426	5213	10326	2	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4191	9317		5.22	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)

Page 77 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
247	5438	10578	4.77	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
366	5546	10688	3.66	2.0E-16	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
368	5548	10689	3.56	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2352	7459	12714	1.04	2.0E-15	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
2352	7459	12715	1.04	2.0E-15	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
3494	8635	13801	0.61	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3494	8635	13802	0.61	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4592	9710		2.53	2.0E-15	AI806335.1	EST_HUMAN	w07f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINEIN. ;
2736	7830		2.46	1.0E-15	AI689984.1	EST_HUMAN	b26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE. ;
2983	8137	13302	1.71	1.0E-15	BE043584.1	EST_HUMAN	h040e02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2999162 5'
3120	8272	13428	1.41	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4337	9459	14597	0.6	1.0E-15	BE182663.1	EST_HUMAN	RC3-HIT0649-100500-022-b05 HIT0649 Homo sapiens cDNA
2644	7742	12995	1.04	9.0E-16	Q39610	SWISSPROT	DYNEIN ALPHA CHAIN, FLAGELLAR OUTER ARM
4481	9600	14739	1.04	9.0E-16	4503168	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
2126	7240		3.12	6.0E-16	AW972611.1	EST_HUMAN	EST384702 IMAGE: ressequences; MAGL Homo sapiens cDNA
1503	6630	11817	1.38	5.0E-16	AJ251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene o80c04.s1 Soares_total Fetus Nb2HFB_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element ;
2641	7739	12992	1.28	5.0E-16	AA992176.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
2359	7466	12721	1.04	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
2359	7466	12722	1.04	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3439	8581	13741	3.97	4.0E-16	Q16653	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4113	9241	14377	5.45	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4113	9241	14378	5.45	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4926	10036		1.02	4.0E-16	AV730833.1	EST_HUMAN	AV730833 HITF Homo sapiens cDNA clone HITFAE09 5'

Page 78 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
128	5326	10472	1.01	3.0E-16	AW022862.1	EST_HUMAN	d145c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
128	5326	10473	1.01	3.0E-16	AW022862.1	EST_HUMAN	d145c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
465	5633		1.3	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434P037 5'
475	5642		2.42	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1465	5592	11780	1.85	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
							ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
2945	8099	13283	4.39	3.0E-16	P03200	SWISSPROT	EST06060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
3506	9042	14202	0.68	3.0E-16	T08169.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
973	9120		1.52	2.0E-16	AL163279.2	NT	Human SSAV-related endogenous retroviral LTR-like element
2650	7748		1.74	2.0E-16	J03081.1	NT	H. sapiens DNA for endogenous retroviral like element
4149	9275	14412	1.25	2.0E-16	X89211.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
180	5374	10513	2.74	1.0E-16	AF200719.1	NT	contains ORF12 OFR repetitive element;
							er39g11.s1 Soares fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to
380	5589		21.64	1.0E-16	AA628592.1	EST_HUMAN	QV0-BN0148-070700-293-e10 BN0148 Homo sapiens cDNA
1973	7090	12319	2.07	1.0E-16	BF327942.1	EST_HUMAN	CM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
3720	8858	14011	2.64	9.0E-17	AW900048.1	EST_HUMAN	QV0-O10032-080300-155-d01 OT0032 Homo sapiens cDNA
1019	5180		2.04	8.0E-17	AW880701.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
3859	9005		0.83	8.0E-17	AL163280.2	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
1470	6597		2.64	7.0E-17	6753087	NT	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
200	5395	10539	6.48	6.0E-17	AW963880.1	EST_HUMAN	yc05h08.t1 Stratiagene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
420	5207	10319	2.67	5.0E-17	T64110.1	EST_HUMAN	Human DNA, SINE repetitive element
1504	6631		1.25	3.0E-17	D14547.1	NT	xd89c09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
2089	7204	12449	1.06	3.0E-17	AW119123.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3177	8328		1.26	3.0E-17	P35410	SWISSPROT	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
3620	8759	13915	1.18	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
3620	8759	13916	1.18	3.0E-17	BE326522.1	EST_HUMAN	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
350	5533	10672	2.53	2.0E-17	AI270080.1	EST_HUMAN	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
351	5533	10672	2.82	2.0E-17	AI270080.1	EST_HUMAN	zg91d04.s1 Soares fetal_heart_Nb1-H19W Homo sapiens cDNA clone IMAGE:399751 3'
989	6136		1.24	2.0E-17	AA722932.1	EST_HUMAN	ZONADHESIN PRECURSOR
2424	7529	12781	1.33	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2424	7529	12782	1.33	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR

Page 79 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2895	8049	13216	6.11	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
749	5905	11061	2.99	1.0E-17	P06183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1723	6850		0.98	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
1778	6904	12112	2.75	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2105	7220	12464	1.28	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2317	7425	12676	1.44	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3554	8695		0.99	1.0E-17	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
4108	9236		7.66	1.0E-17	R05942.1	EST_HUMAN	(UBE2D3) genes, complete cds
5185	10282		1.15	1.0E-17	AA299037.1	EST_HUMAN	Y30e07.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:128388 5'
3765	8902	14054	1.61	8.0E-18	4758977	NT	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retinoblastoma-related pol
346	5529	10666	40.25	7.0E-18	AW316976.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
346	5529	10667	40.25	7.0E-18	AW316976.1	EST_HUMAN	xx10504.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
3277	8428	13587	1.08	6.0E-18	X71791.2	NT	RIBOSOMAL PROTEIN L4 (HUMAN);
4712	9828		3.18	6.0E-18	P52181	SWISSPROT	RIBOSOMAL PROTEIN L4 (HUMAN);
1149	6285	11450	12.11	5.0E-18	A1280214.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
120	5320	10463	1.1	4.0E-18	BE044076.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
120	5320	10494	1.1	4.0E-18	BE044076.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
1731	6858	12082	30.81	4.0E-18	AA621814.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
850	6001	11173	15.02	3.0E-18	AA814186.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
931	6079	11247	2.19	3.0E-18	BE088634.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
3923	9069	14218	0.98	3.0E-18	AL163247.2	NT	RIBOSOMAL PROTEIN L4 (HUMAN);
248	5439	10579	3.23	2.0E-18	AW836820.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
1154	6280		198.34	2.0E-18	BE256097.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
3100	8253	13403	1	2.0E-18	Q39575	SWISSPROT	RIBOSOMAL PROTEIN L4 (HUMAN);
							q24f11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
							KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
							q23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN
							P46782 40S RIBOSOMAL PROTEIN S5.;
							CMO-B10690-210300-288-q07 BT0690 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C047
							QV1-LT0036-150200-070-e07 LT0036 Homo sapiens cDNA
							60114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3365044 5'
							DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM

Page 80 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4393	9513		0.61	1.0E-18	T95406.1	EST_HUMAN	ye49g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element;
544	5710	10846	4.89	9.0E-19	AA281981.1	EST_HUMAN	z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
545	5710	10846	2.47	9.0E-19	AA281981.1	EST_HUMAN	MER19 repetitive element;
1050	6191		2.5	8.0E-19	AW074902.1	EST_HUMAN	z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
2226	7338	12592	2.58	7.0E-19	4758139	NT	MER19 repetitive element;
3760	8997		1.22	6.0E-19	AW852930.1	EST_HUMAN	EST1387007 IMAGE resequences, MAGN Homo sapiens cDNA
4442	9361	14703	1.35	6.0E-19	P34988	SWISSPROT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
4442	9361	14704	1.35	6.0E-19	P34988	SWISSPROT	PM0-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4768	9881		1.48	6.0E-19	AJ271735.1	NT	OLFACTORY RECEPTOR 6 (M50)
5009	10112	15243	1.03	6.0E-19	AL120817.1	EST_HUMAN	OLFACTORY RECEPTOR 6 (M50)
553	5718	10850	0.84	4.0E-19	AB007970.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2943	7741	12994	1.16	4.0E-19	BF697382.1	EST_HUMAN	DKFZp762F192.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762F192.5
5105	10206		0.88	4.0E-19	AL163208.2	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
3831	8967	14120	1.04	3.0E-19	Q28997	SWISSPROT	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'
4260	9385	14521	0.83	3.0E-19	Q43900	SWISSPROT	Homo sapiens chromosome 21 segment HS21C008
4260	9385	14522	0.83	3.0E-19	Q43900	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4425	9545	14683	1.07	3.0E-19	AV708136.1	EST_HUMAN	BETA-2 ADRENERGIC RECEPTOR
2529	7632	12880	33.58	2.0E-19	AL163201.2	NT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4424	9544		1.43	2.0E-19	AI311783.1	EST_HUMAN	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
481	5849		2.72	1.0E-19	BE408611.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
2146	7260	12507	1.19	1.0E-19	H30795.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
2879	7776		1.37	1.0E-19	D38044.1	NT	qc91a02.x1 NCI_CGAP_Kh5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386
2810	7966		5.49	1.0E-19	4758977	NT	POLYEN V GENE
3382	8526	13688	1.25	1.0E-19	AA834987.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
3259	8408	13571	0.89	7.0E-20	BF326455.1	EST_HUMAN	ye79g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains
3542	8683	13846	3.35	6.0E-20	P39188	SWISSPROT	MER10 repetitive element;
							Human gene for Ah-receptor, exon 7-9
							Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
							ej49b12.g1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12
							MER37 repetitive element;
							PM4-AN0096-050900-003-e04 AN0096 Homo sapiens cDNA
							ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY

Page 81 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4246	9371	14504	2.93	6.0E-20	BE622434.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4568	9886		1.46	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTG Homo sapiens cDNA clone HCBTA01 5'
1632	6761	11957	1.38	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4182	9308	14445	1.36	3.0E-20	P23279	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4594	9712	14849	0.93	3.0E-20	AA037616.1	EST_HUMAN	zK36b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element ;
831	5983		20.39	2.0E-20	AW303868.1	EST_HUMAN	xr24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW_RS5_MOUSE
1112	6250	11413	2.96	2.0E-20	AA516335.1	EST_HUMAN	ng68h09.s1 NCL_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
1112	6250	11414	2.96	2.0E-20	AA516335.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN ;
2778	5983		12.94	2.0E-20	AW303868.1	EST_HUMAN	ng68h09.s1 NCL_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
4923	10033	15174	3.78	2.0E-20	Q28983	SWISSPROT	G1224066 ORF2: FUNCTION UNKNOWN ;
4923	10033	15175	3.78	2.0E-20	Q28983	SWISSPROT	xr24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW_RS5_MOUSE
5124	10225		1.15	2.0E-20	5174538	NT	ZONADHESIN PRECURSOR
2010	7874	12364	1.86	1.0E-20	AA281961.1	EST_HUMAN	ZONADHESIN PRECURSOR
4416	9536	14676	0.94	1.0E-20	BF115158.1	EST_HUMAN	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
2878	8032		0.97	9.0E-21	AJ003514.1	EST_HUMAN	z111d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
2081	7177	12415	2.96	7.0E-21	P15800	SWISSPROT	repetitive element ;
2061	7177	12416	2.96	7.0E-21	P15800	SWISSPROT	repetitive element ;
3679	8818	13975	0.6	7.0E-21	AL163300.2	NT	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIpl12-8J21
4231	9356		8.25	7.0E-21	AA046502.1	EST_HUMAN	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4079	9209	14346	0.6	6.0E-21	BE408611.1	EST_HUMAN	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
925	6073	11241	0.69	5.0E-21	5902031	NT	Homo sapiens chromosome 21 segment HS21C100
4341	9463	14600	2.97	5.0E-21	BE968839.1	EST_HUMAN	zK67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
4770	9883	15030	7.42	5.0E-21	4885474	NT	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
1747	6873	12078	1.2	4.0E-21	AA970713.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
2253	7363	12619	1.05	3.0E-21	AL163201.2	NT	601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
3052	8205	13360	3.39	3.0E-21	AJ007973.1	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
							cc86e08.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530
							PMS3 mRNA ; contains ORF.t1 ORF repetitive element ;
							Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens LGMD2B gene

Page 82 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
141	5338		19.37	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
936	6084	11249	0.95	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
936	6084	11250	0.95	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1217	6349		2.35	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-14109-011-h06 BT0311 Homo sapiens cDNA
2601	7701	12956	1.72	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2601	7701	12957	1.72	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
1259	6388	11565	1.63	1.0E-21	AA557657.1	EST_HUMAN	n146c04.s1 NCI CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
1410	6537		2.71	1.0E-21	AI601284.1	EST_HUMAN	MER29 repetitive element ;
4388	9508	14650	2.25	9.0E-22	AI702438.1	EST_HUMAN	ar88d12.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
950	6098		5.92	8.0E-22	BE144748.1	EST_HUMAN	zb24a03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2266204 3' similar to TR:Q15408 Q15408
684	5824	10982	4.97	7.0E-22	AL163248.2	NT	NEUTRAL PROTEASE LARGE SUBUNIT ;
4257	9382	14515	1.94	7.0E-22	Q61838	SWISSPROT	CMC-HT0179-281089-078-h05 HT0179 Homo sapiens cDNA
5020	10122	19254	1.06	7.0E-22	AB008681.1	NT	Homo sapiens chromosome 21 segment HS21C046
4035	9166	14308	1.01	8.0E-22	AA405040.1	EST_HUMAN	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
3614	8753		1.26	4.0E-22	AJ271735.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
960	6108		0.83	3.0E-22	AI469679.1	EST_HUMAN	zu65d10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742867 5'
2535	7638	12886	2.31	3.0E-22	AI859038.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
3650	8799		1.46	3.0E-22	D14718.1	NT	hm14h10.x1 NCI CGAP_Cot4 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:L19593 HIGH
4769	9882	15029	2.86	3.0E-22	AI090125.1	EST_HUMAN	AFFINITY INTERLEUKIN-3 RECEPTOR B (HUMAN); contains L1.11 L1 repetitive element ;
1957	7074		1.38	2.0E-22	N21942.1	EST_HUMAN	wf66b04.x1 NCI CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN
2495	7589	12847	1.32	2.0E-22	P24916	SWISSPROT	P46778 60S RIBOSOMAL PROTEIN L21. ;
3401	8545	13704	3.77	2.0E-22	8394043	NT	Human chromosomal protein HMGI related gene
4203	9328	14460	1.73	2.0E-22	AW817794.1	EST_HUMAN	qb28c07.x1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:1697680 3' similar to
1899	7009	12229	1.11	1.0E-22	AW865517.1	EST_HUMAN	contains MER12.12 MER12 repetitive element ;
3392	8536	13697	1.42	1.0E-22	D14547.1	NT	yz73405.s1 Soares_melanocyte_2NBHM Homo sapiens cDNA clone IMAGE:267369 3'
3567	8608	13868	0.6	8.0E-23	AF198349.1	NT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3292	8439		2.2	7.0E-23	AV647246.1	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
3415	8558		1.77	8.0E-23	AF198333.1	NT	PM1-ST0262-261189-001-d12 ST0262 Homo sapiens cDNA
4242	9367	14500	1.08	6.0E-23	AL163249.2	NT	PM4-SN0020-010400-009-t02 SN0020 Homo sapiens cDNA
							Human DNA, SINE repetitive element
							Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
							AV647246 GLC Homo sapiens cDNA clone GLCAW037 3'
							Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
							Homo sapiens chromosome 21 segment HS21C049



Page 83 of 214  
Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
665	5825	10963	3.85	2.0E-23	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1144	7868		3.08	2.0E-23	M59270.1	NT	Human matrix Gla protein (MGF) gene, complete cds
2756	7850	13105	1.39	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2756	7850	13106	1.39	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3353	8498		0.91	2.0E-23	AI201458.1	EST_HUMAN	q973f1.1 x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537
3696	8834		3.7	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
3949	9084	14237	2.51	2.0E-23	H59931.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3949	9084	14238	2.51	2.0E-23	H59931.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA clone IMAGE:205418 5'
4503	9622	14764	1.68	1.0E-23	AL163252.2	NT	y16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
4731	9844		5.27	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C052
551	5716		3.98	9.0E-24	AA663213.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
4617	9735	14872	1.03	8.0E-24	P23269	SWISSPROT	ab75a08.s1 Stratiogene fetal refina 937202 Homo sapiens cDNA clone IMAGE:862758 3' similar to
4617	9735	14873	1.03	8.0E-24	P23269	SWISSPROT	TR:E19922 E19922 CA PROTEIN ;
3850	8988		1.12	7.0E-24	AW937954.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN I3
704	5861		2.18	6.0E-24	AB001421.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
839	5991	11159	14.22	6.0E-24	AL163249.2	NT	QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA
3943	9079	14232	7.47	5.0E-24	AJ229043.1	NT	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds
5075	10176	16310	1.58	3.0E-24	F08337.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
2326	7434	12687	1.07	2.0E-24	AA167539.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3778	8913		0.88	2.0E-24	AW888189.1	EST_HUMAN	HSC2RC061 normalized infant brain cDNA Homo sapiens cDNA clone c-zrc06
1709	6837	12038	3.43	1.0E-24	7706340	NT	zP11109.r1 Stratiogene fetal refina 937202 Homo sapiens cDNA clone IMAGE:609161 5'
2634	7732		1	1.0E-24	AW820194.1	EST_HUMAN	RC3-NN0088-090500-021-b03 NN0088 Homo sapiens cDNA
2992	8147	13307	0.65	1.0E-24	D86423.1	NT	Homo sapiens CGI-127 protein (LOC51646), mRNA
4244	9369		1.97	1.0E-24	AF143313.1	NT	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
5182	10279	15417	1.03	9.0E-25	AW857136.1	EST_HUMAN	Mus musculus PTEN (PTEN) gene, exon 2
4982	10090	15223	3.25	7.0E-25	AA183944.1	EST_HUMAN	Homo sapiens PTEN (PTEN) gene, exon 2
1684	6792	11988	1.32	5.0E-25	AW850271.1	EST_HUMAN	RC1-C10302-040400-017-g02 CT0302 Homo sapiens cDNA
1459	6596	11774	1.45	4.0E-25	T88107.1	EST_HUMAN	ne92e10.s1 NCL CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1 b2
3383	8527		3.48	4.0E-25	AW887871.1	EST_HUMAN	MER1 repetitive element ;
4294	9416		3.86	4.0E-25	BE170957.1	EST_HUMAN	IL3-CT0219-161199-031-DD4 CT0219 Homo sapiens cDNA
3301	8448	13610	2.96	3.0E-25	8923321	NT	y656f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
							PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
							QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
							Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA

Page 84 of 214  
Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3301	8448	13611	2.96	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
1354	6483	11663	3.09	2.0E-25	5032159	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2285	7394	12645	4.17	2.0E-25	BE88016.1	EST_HUMAN	601511330F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2792	7617	12866	8.6	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4161	9287	14422	1.6	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4161	9287	14423	1.6	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
362	5542	10684	0.96	1.0E-26	AL040229.1	EST_HUMAN	DKFZp434H0313.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313 5'
1252	6382		1.96	1.0E-25	9635487	NT	Human endogenous retrovirus, complete genome
2412	7518	12768	2.79	1.0E-25	Q06055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4828	9940	15082	2.58	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-H09 HT0454 Homo sapiens cDNA
2455	7560	12812	1.08	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
1590	6719	11908	1.3	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3953	9088	14242	1.18	7.0E-26	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4131	9259	14396	1.87	7.0E-26	AW340153.1	EST_HUMAN	hd02e12.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2908365 3'
2207	7319	12570	2.86	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tryptophan gene families
3328	8474	13637	1	6.0E-26	AA206131.1	EST_HUMAN	z052h04.r1 Stratagene neuroepithelium (#9377231) Homo sapiens cDNA clone IMAGE:645271 5'
1179	6314	11482	1.72	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;
1179	6314	11483	1.72	5.0E-26	AI708235.1	EST_HUMAN	ec38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;
1658	6687		1.21	4.0E-26	AA325548.1	EST_HUMAN	EST33446 Embryo, 12 week II Homo sapiens cDNA 5' end
1770	6896	12102	0.96	3.0E-26	D14647.1	NT	Human DNA, SINE repetitive element
2004	7121	12357	1.15	3.0E-26	AL045855.2	EST_HUMAN	DKFZp434I066.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I066 5'
2026	7143		2.18	3.0E-26	AA115695.1	EST_HUMAN	zn30c08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3759	8896	14046	1.25	3.0E-26	AA152464.1	EST_HUMAN	z030f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 ;
3759	8896	14047	1.25	3.0E-26	AA152464.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
680	5838	10978	5.51	2.0E-26	AL163282.2	NT	z030f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 ;
1879	6999		1.73	2.0E-26	AL038099.2	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
3216	8367	13531	5.31	2.0E-26	X86694.1	NT	Homo sapiens chromosome 21 segment HS21C082 DKFZp566L171.1 st 568 (synonym: htk2) Homo sapiens cDNA clone DKFZp566L171 3' M. musculus mRNA for astrocytic phosphoprotein, PEA-15

Page 85 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
132	5330	10475	40.29	1.0E-26	BE170371.1	EST_HUMAN	QV4-HT0538-020300-123-a02 HT0538 Homo sapiens cDNA
2632	7635	12883	0.95	1.0E-26	BE814995.1	EST_HUMAN	MR2-BN0114-240500-030-g07 BN0114 Homo sapiens cDNA
2648	7746		25.15	1.0E-28	AF261085.1	NT	Homo sapiens glycerate dehydrogenase (GADPH) mRNA, complete cds
10	5221	10333	3.06	8.0E-27	AI831462.1	EST_HUMAN	wf49-c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
556	5721		4.14	8.0E-27	AL163227.2	NT	THR repetitive element;
1424	6551	11732	72.92	8.0E-27	AW162737.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1424	6551	11733	72.92	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
2149	7262	12510	1.86	8.0E-27	AW864776.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
3168	8317	13479	2.34	8.0E-27	P12236	SWISSPROT	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
682	6940		2.02	7.0E-27	Z70684.1	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
5074	10175		2.28	7.0E-27	AW626172.1	EST_HUMAN	PM2-SN0018-220300-002-a07 SN0018 Homo sapiens cDNA
2362	7469	12724	2.17	4.0E-27	D25303.1	NT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE
2035	7153	12393	2.58	3.0E-27	X60658.1	NT	NUCLEOTIDE TRANSLATOR 3) (ANT 3)
4245	9370	14503	1.31	3.0E-27	BE071924.1	EST_HUMAN	Human endogenous retroviral element HC2
40	5251	10369	28.98	2.0E-27	AF054187.1	NT	h51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
1902	7021		45.43	2.0E-27	AA565345.1	EST_HUMAN	O76040 ORF2: FUNCTION UNKNOWN. ;
3085	8238		10.92	2.0E-27	AW626172.1	EST_HUMAN	Human mRNA for integrin alpha subunit, complete cds
3209	8360	13521	2.17	2.0E-27	AF111167.2	NT	Rattus RY3A3 mRNA for a potential ligand-binding protein
3209	8360	13522	2.17	2.0E-27	AF111167.2	NT	PM0-BT0527-090100-001-411 BT0527 Homo sapiens cDNA
435	5604		1.48	1.0E-27	AL163246.2	NT	Homo sapiens alpha NAC mRNA, complete cds
997	6143	11311	1.58	1.0E-27	AB026898.1	NT	rk01b10.s1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
1711	6839	12040	0.87	1.0E-27	4827059	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
4058	9188		0.93	1.0E-27	BE350127.1	EST_HUMAN	h51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
							O76040 ORF2: FUNCTION UNKNOWN. ;
							Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
							Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
							Homo sapiens chromosome 21 segment HS21C046
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
							Homo sapiens Xylulokinase (H. Influenzae) homolog (XylB) mRNA
							h108g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
							MER29 repetitive element;

Page 86 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
137	5333		1.86	9.0E-28	BE348399.1	EST_HUMAN	hw17c11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3193188 3' similar to TR:Q07314 Q07314
309	5495	10635	2.48	9.0E-28	AU126260.1	EST_HUMAN	SECRETED NEUREXIN II-ALPHA-C PRECURSOR, [3] TR:Q07280 TR:Q07313;
5144	10244	15381	1.58	9.0E-28	AI590115.1	EST_HUMAN	to12b09.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFF repetitive element;
5144	10244	15382	1.58	9.0E-28	AI590115.1	EST_HUMAN	to12b09.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFF repetitive element;
1183	6318	11486	12.92	7.0E-28	AU142750.1	EST_HUMAN	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
316	5502		2.47	5.0E-28	AI921003.1	EST_HUMAN	wo18c07.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2465692 3' similar to contains THR.b1 THR repetitive element;
3984	9118	14285	1.27	5.0E-28	R79792.1	EST_HUMAN	y89f10.t1 Scores placenta Nb2-IP Homo sapiens cDNA clone IMAGE:146443 5'
2590	7691	12946	1.79	4.0E-28	AW195066.1	EST_HUMAN	xs33c09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95;
2946	8100	13264	1.43	4.0E-28	4505316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
3084	8237	13387	2.63	4.0E-28	BE409100.1	EST_HUMAN	607300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
1287	6416		1.61	3.0E-28	AF155382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
6100	10200		0.92	3.0E-28	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S3A2 to TORBV12S2 region
84	5293	10433	9.51	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1167	6302	11468	7.61	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2450	7554	12806	2.08	2.0E-28	AI348634.1	EST_HUMAN	qs36b06.x1 NCL_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element;
3343	8489	13655	0.62	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1488	6615	11803	2.07	1.0E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2202	7314	12566	1.03	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-503 BT0821 Homo sapiens cDNA
4541	9689		0.98	1.0E-28	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
1616	6744	11939	1.25	7.0E-28	AW96447.1	EST_HUMAN	EST378521 MAGI resequences, MAGI Homo sapiens cDNA
593	5755	10883	8.3	6.0E-29	AI936748.1	EST_HUMAN	wp68b01.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
4984	10092		1.32	5.0E-29	AL163203.2	NT	O15475 UNNAMED HERV-H PROTEIN, contains LTR7.b1 LTR7 repetitive element;
3217	8368		2.16	4.0E-29	AI752367.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
4392	9512	14654	1.32	3.0E-29	AB042297.1	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
4701	9817	14985	1.06	3.0E-29	BF333236.1	EST_HUMAN	Homo sapiens PTS gene for 8-pyruvyltetrahydropterin synthase, complete cds
							QV1-BT0821-120900-360-503 BT0821 Homo sapiens cDNA

Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
492	5539	10794	2.02	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds
492	5539	10795	2.02	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds
1547	6675	11860	5.63	2.0E-29	AI963604.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN;
1547	6675	11861	5.63	2.0E-29	AI963604.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN;
4253	9378	14509	2.04	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1530	6657	12117	1.11	7.0E-30	BE091133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1783	6909	12117	1.11	8.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3173	8324	13485	3.1	6.0E-30	BE008028.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
4724	8324	13485	0.94	8.0E-30	BE008028.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
3988	9122	14269	30.82	5.0E-30	AI399992.1	EST_HUMAN	ig92g03.x1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element;
2128	7242	12484	1.89	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
2128	7242	12485	1.89	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA
1153	6289		2.88	3.0E-30	AI338551.1	EST_HUMAN	qq93c05.x1 Soares_tbal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element;
3738	8876	14027	0.93	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
674	5832	10972	1.27	2.0E-30	AW857315.1	EST_HUMAN	GM0-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA
1085	6224		1.82	2.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
1489	6616	11804	3.7	2.0E-30	BE175877.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2676	7773	13024	4.7	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2885	8039	13204	7	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3768	8905	14058	2.23	2.0E-30	AW206581.1	EST_HUMAN	UI-H-B11-afb-c-12-Q-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4745	9858	15008	3.09	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4745	9858	15007	3.09	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
284	5473	10515	14.45	1.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TF-ujwara) Homo sapiens cDNA clone GEN-570C01 5'
536	5702	10835	7.24	1.0E-30	AW468897.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.13 MER1 repetitive element;
714	5871	11018	3.43	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2104	7305	12556	2.77	1.0E-30	AA664377.1	EST_HUMAN	ac77b08.s1 Stragene lung (#637210) Homo sapiens cDNA clone IMAGE:968599 3'
2438	7542	12795	1.44	1.0E-30	BF347728.1	EST_HUMAN	602022560F1 NCI CGAP_Bm57 Homo sapiens cDNA clone IMAGE:4157991 5'
2974	8128	13291	1.24	1.0E-30	5803091	NT	Homo sapiens methionine aminopeptidase; eIF-2-associated p67 (MNPEP), mRNA
3026	8180	13336	0.87	1.0E-30	AA315045.1	EST_HUMAN	EST188868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end

Page 88 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3746	8884	14034	0.6	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stragene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
3746	8884	14035	0.6	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stragene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
1078	6218	11383	6.59	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2390	7498		8.16	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
4895	10006	15150	0.98	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
4895	10006	15151	0.98	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
709	5866		1.37	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2629	7727	12882	2.1	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2629	7727	12883	2.1	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
3656	8795		2.31	8.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
189	5384	10526	2.84	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
189	5384	10527	2.84	6.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
594	5756		3.26	4.0E-31	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1624	6752	11845	1.08	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
1829	6952		1.27	4.0E-31	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2750	7844		1.87	4.0E-31	5730038	NT	Homo sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
2558	7660	12913	2.37	3.0E-31	600587.1	NT	Homo sapiens SEC63, endoplasmic reticulum transcon component (S. cerevisiae) like (SEC63L), mRNA
1920	7039	12260	1.98	2.0E-31	AW838171.1	EST_HUMAN	GV2.1.T0051-261300-111-103.L.T0051 Homo sapiens cDNA
2196	7308	12558	1.54	2.0E-31	AI393386.1	EST_HUMAN	tg44g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2321	7429	12682	0.98	2.0E-31	AL119245.1	EST_HUMAN	DKFZp781G1513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781G1513 5'
2418	7523	12775	3.48	2.0E-31	AA458824.1	EST_HUMAN	aa88f11.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR12 THR repetitive element;
15	5226	10339	5.7	1.0E-31	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
1676	6805	12000	7.67	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1676	6805	12001	7.67	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1676	6805	12002	7.67	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4605	9723	14857	1.1	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5'
4605	9723	14858	1.1	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5'
2828	7983		1.08	9.0E-32	U60871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds

Page 89 of 214

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2069	7185	12426	6.64	8.0E-32	AI056770.1	EST_HUMAN	oz15a09.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
4829	9941	15083	0.94	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P146)
1030	9177	11342	48.23	5.0E-32	AF116827.1	NT	Homo sapiens PRO1181 mRNA, complete cds
932	6080		1.85	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
455	5623	10766	3.06	3.0E-32	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1467	5594	11783	16.89	3.0E-32	AV731500.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK07 5'
2873	8027	13194	0.64	3.0E-32		NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2873	8027	13195	0.64	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2638	7736		1.98	1.0E-32	D84430.1	NT	Homo sapiens mRNA for phenylalanine tRNA synthetase, complete cds
3067	8220		1.47	1.0E-32	BE749209.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
3492	8604		5.35	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3192216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11.;
60	5271	10403	5.57	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
60	5271	10404	5.57	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2143	7257	12503	1.13	7.0E-33	AI590115.1	EST_HUMAN	to12b09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR repetitive element;
2610	7709		5.84	7.0E-33	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
3226	8376		13.21	7.0E-33	AW971307.1	EST_HUMAN	EST383399 MAGI3 resequences, MAGI3 Homo sapiens cDNA
3718	8856		1.06	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1787	6913		1.49	5.0E-33	BF373515.1	EST_HUMAN	QV1-FT0169-100700-271-s02 FT0169 Homo sapiens cDNA
1905	7024	12243	2.06	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1905	7024	12244	2.06	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2251	7361		1.73	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4032	9163	14305	0.86	5.0E-33	AB014599.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
1129	6266		1.69	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2117	7232	12474	3.01	4.0E-33	4756987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2397	7503		2.47	4.0E-33	AA626621.1	EST_HUMAN	ab61b1.r1 Striatum lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:644317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element;
2516	7620	12668	1.28	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4462	9581	14719	1.67	4.0E-33	AW263349.1	EST_HUMAN	UHF-B12-ah1-c-03-0-UI.st1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'

Page 90 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1090	6229		4.74	3.0E-33	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
1091	6229		4.22	3.0E-33	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
2426	7940		1.24	3.0E-33	AV647851.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone GLC9CF09 3'
16	5227		1.23	2.0E-33	AI160188.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFF repetitive element;
101	5227		1.89	2.0E-33	AI160188.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFF repetitive element;
4397	9517		3.87	2.0E-33	BE159039.1	EST_HUMAN	MRO-HT0405-160300-202-408 HT0405 Homo sapiens cDNA
4970	10078	15215	15.38	2.0E-33	AA626683.1	EST_HUMAN	ab51g11.1 Striatogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5078	10179	15314	1.37	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5078	10179	15315	1.37	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
8	5219		1.37	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2151	7264	12512	1.17	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
4475	9594	14733	0.91	8.0E-34	BE062570.1	EST_HUMAN	QV2-BT0258-071299-019-g07 BT0258 Homo sapiens cDNA
1456	6583	11771	1.63	7.0E-34	T70845.1	EST_HUMAN	y015a05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
470	5637	10778	1.44	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
470	5637	10779	1.44	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
1890	7010		2.57	5.0E-34	7706500	NT	Homo sapiens Npw35-binding protein NpwBP (LOC51729), mRNA
5044	10146	15275	4.3	5.0E-34	U30883.1	NT	Human splicing factor SRP55-1 (SRP-55) mRNA, complete cds
5127	10227		1.06	5.0E-34	N98282.1	EST_HUMAN	Human splicing factor SRP55-1 (SRP-55) mRNA, complete cds
1999	7116	12352	1.33	4.0E-34	AI804697.1	EST_HUMAN	z027g11.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:293828 5'
2681	7778	13028	1.69	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10989 (FLJ10989), mRNA
3152	8303	13493	1.02	4.0E-34	5803166	NT	Homo sapiens splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA
1520	6647	11834	18.47	1.0E-34	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3651	8760	13944	1.42	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4045	9176	14317	0.75	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4045	9176	14318	0.75	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4459	9578		2.13	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-016-h08 BT0506 Homo sapiens cDNA



Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4909	10019	15163	1.45	1.0E-34	BF509718.1	EST_HUMAN	UI-H-B14-apb-h-04-0-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086839 3'
4909	10019	15164	1.45	1.0E-34	BF509718.1	EST_HUMAN	UI-H-B14-apb-h-04-0-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086839 3'
3623	8762	13918	1.31	8.0E-35	AW683302.1	EST_HUMAN	h77b06.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988787 5'
223	5416		39.92	8.0E-35	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
1749	6875	12080	2.13	8.0E-35	BF588937.1	EST_HUMAN	ne33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
1749	6875	12081	2.13	8.0E-35	BF588937.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA.
4836	9948	16082	2.74	8.0E-35	BF183195.1	EST_HUMAN	ne33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
1420	6547	11728	0.98	6.0E-35	AA757115.1	EST_HUMAN	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
1970	7087	12314	5.54	6.0E-35	6005975	NT	ah53h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'
4027	9158	14301	0.66	6.0E-35	AW297191.1	EST_HUMAN	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
1724	6851	12055	1.36	5.0E-35	X63392.1	NT	UI-H-BW0-ajd-d-09-0-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
2745	7839	13084	1.34	5.0E-35	AB007666.2	NT	H sapiens immunoglobulin kappa light chain variable region L14
2980	8135	13298	1.38	5.0E-35	5912639	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4387	9507	14649	1.91	6.0E-35	AF023268.1	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
1444	6572	11759	28.26	4.0E-35	BE257907.1	EST_HUMAN	Homo sapiens cdk2 kinase (CLK2), propln1, cde1, glucocorticoidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocorticoidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
1830	6853	12174	8.39	4.0E-35	H91183.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1592	6721	11911	40.56	3.0E-35	BE268182.1	EST_HUMAN	yu08a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element;
2312	7421		1.77	3.0E-35	AF224492.1	NT	601125280F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
104	7883	10450	1.29	2.0E-35	N88995.1	EST_HUMAN	Homo sapiens phospholipid scramblase 1 gene, complete cds
1190	6324	11492	1.28	2.0E-35	T11909.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
2200	7312	12564	2.32	2.0E-35	AB018413.1	NT	A971F Heart Homo sapiens cDNA clone A971
2645	7743	12896	1.9	2.0E-35	AW665005.1	EST_HUMAN	Homo sapiens mRNA for Gab2, complete cds
3293	8440	13601	0.62	2.0E-35	5912459	NT	h86a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879166 3' similar to SW:TR12_HUMAN_Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12;
3293	8440	13602	0.62	2.0E-35	5912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3543	8684		1.04	2.0E-35	AB020702.1	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3887	9023	14180	0.77	2.0E-35	BE247575.1	EST_HUMAN	Homo sapiens mRNA for KIAA0695 protein, partial cds
							TCBAP2E-4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328

Page 92 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3987	9023	14181	0.77	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Bayot-HGSC project TCBA Homo sapiens cDNA clone TCBAP4328
4940	9758		2.94	2.0E-35	H49239.1	EST_HUMAN	Yq19a12.1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:274079 5'
45	5257	10378	4.39	1.0E-35	AA631949.1	EST_HUMAN	Imf16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
45	5257	10379	4.38	1.0E-35	AA631949.1	EST_HUMAN	Imf16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
751	5907	11052	16.82	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-008-d12 ST0162 Homo sapiens cDNA
751	5907	11053	16.82	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-008-d12 ST0162 Homo sapiens cDNA
910	6060		1.46	1.0E-35	T87947.1	EST_HUMAN	Y493a01.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
2573	7816	12865	3.29	1.0E-35	7705994	NT	Homo sapiens hypophyseal protein (LOC51233), mRNA
2729	7824	13079	1.24	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCLCGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
2729	7824	13080	1.24	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCLCGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
3121	8273	13429	1.25	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCB1L) mRNA
3142	8293	13450	3.15	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEFO6 3'
3142	8293	13451	3.15	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEFO6 3'
4400	9520	14661	3.82	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4400	9520	14661	3.82	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
3960	9095	14247	0.96	9.0E-36	AW821707.1	EST_HUMAN	RC3-ST0315-180200-013-f12 ST0315 Homo sapiens cDNA
2896	8050	13217	1.52	7.0E-36	AW857678.1	EST_HUMAN	GM1-CT0315-081298-053-d07 CT0315 Homo sapiens cDNA
3094	8247		4.75	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
2005	7122	12358	1.46	6.0E-36	7706622	NT	Homo sapiens ninjurin 2 (NINJ2), mRNA
2395	7501		4	6.0E-36	AB036346.1	NT	Homo sapiens TCL6 gene, exon 12
3617	8756	13912	0.81	6.0E-36	BF515101.1	EST_HUMAN	U1-HBW1-ant-c-12-0-U1.s1 NCLCGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
4943	10053	15191	1.29	6.0E-36	AB030501.1	NT	Rattus norvegicus mRNA for DLG6 gamma, complete cds
133	5331	10476	11.17	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2714	7809	13063	52.37	5.0E-36	BE388436.1	EST_HUMAN	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
3596	8735	13687	1.6	5.0E-36	AL163209.2	NT	Homo sapiens chromosome 21 segment HSZ1C009
4755	9868	15017	1.95	5.0E-36	5729729	NT	Homo sapiens API6-like 1 (API6L1), mRNA
4755	9868	15018	1.95	5.0E-36	5729729	NT	Homo sapiens API6-like 1 (API6L1), mRNA
1227	6359	11529	2.69	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1453	6580	11769	1.93	4.0E-36	P10266	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID, NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1657	6785	11879	1.72	4.0E-36	BE362574.1	EST_HUMAN	601298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
2204	7316		5.27	4.0E-36	AW247772.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3335	8481	13647	1.66	4.0E-36	BE369299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3335	8481	13648	1.86	4.0E-36	BE369299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
4719	9833	14977	0.63	4.0E-36	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5110	10211	15348	0.74	4.0E-36	AA905361.1	EST_HUMAN	ok05b11 s1 Soares_NFL_T_GBC_S7 Homo sapiens cDNA clone IMAGE:1506909 3' similar to SW:D3HL_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
694	5851	10996	2.64	3.0E-36	AF099810.1	NT	Homo sapiens neuraxin III-alpha gene, partial cds
1512	6839	11828	1.43	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1512	6839	11827	1.43	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
2273	7383	12631	1.23	3.0E-36	7662401	NT	Homo sapiens KIAA00952 protein (KIAA00952), mRNA
4479	9599	14738	7.19	3.0E-36	10181139	EST_HUMAN	Mus musculus junctophilin 1 (Jp1-pending), mRNA
3149	8300	13460	5.87	2.0E-36	BE259267.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342708 5'
4939	10049	15187	8.66	2.0E-36	AW880378.1	EST_HUMAN	QV0-OT0030-240300-174-H04 OT0030 Homo sapiens cDNA
886	6036	11207	1.67	1.0E-36	BE408310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2129	7243	12486	1.08	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-H07 HT0217 Homo sapiens cDNA
2129	7243	12487	1.08	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-H07 HT0217 Homo sapiens cDNA
2185	7288	12546	1.32	1.0E-36	BF673781.1	EST_HUMAN	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272889 5'
3326	8473		1.34	1.0E-36	AF156862.1	NT	Homo sapiens human endogenous retrovirus W provC8-19 protease (pro) gene, partial cds
1288	6417		3.18	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E0422 5'
1756	6882	12088	0.95	7.0E-37	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1756	6882	12089	0.95	7.0E-37	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
2401	7507	12756	2.5	4.0E-37	AA702794.1	EST_HUMAN	z190504.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
2012	7129	12366	1.96	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2012	7129	12367	1.96	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2463	7587		4.6	3.0E-37	AW991150.1	EST_HUMAN	EST373222 IMAGE resequences, MAGF Homo sapiens cDNA
2934	8088		3.51	3.0E-37	AW991150.1	EST_HUMAN	EST373222 IMAGE resequences, MAGF Homo sapiens cDNA
379	5588	10733	1.65	2.0E-37	DB9790.1	NT	Homo sapiens mRNA for AML1, complete cds
379	5588	10734	1.65	2.0E-37	DB9790.1	NT	Homo sapiens mRNA for AML1, complete cds
1082	6221	11387	2.12	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'

Page 94 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1082	6221	11388	2.12	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 5'
3870	9006	14162	5.62	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrolendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4224	9349	14482	0.68	2.0E-37	4826885	NT	Homo sapiens DEAD/1 (Asp-Glu-Ala-Asp/his) box polypeptide 1 (DDX1) mRNA
2081	7197	12442	3.65	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
3180	8331		1.18	1.0E-37	AW882082.1	EST_HUMAN	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA
3934	9070	14226	0.78	1.0E-37	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4918	10028	15170	2.24	1.0E-37	BF371719.1	EST_HUMAN	QV0-FN0180-280700-318-ct10 FN0180 Homo sapiens cDNA
1224	6366	11526	1.79	8.0E-38	11436955	NT	Homo sapiens Gb2-associated binder 2 (KIAA0571), mRNA
2489	7573	12826	1.23	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153992 5'
2165	7278	12525	3.81	7.0E-38	AW972825.1	EST_HUMAN	EST384920 IMAGE resequencing, MAGL Homo sapiens cDNA
3073	8226	13377	1.1	7.0E-38	AW884259.1	EST_HUMAN	GV3-OT0064-060400-144-09 OT0064 Homo sapiens cDNA
4200	9326	14466	0.82	7.0E-38	H19092.1	EST_HUMAN	yn51107.r1 Soares adult brain N255H955Y Homo sapiens cDNA clone IMAGE:171873 5'
3014	8168	13326	1.99	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855348 5'
725	5881	11029	1.5	5.0E-38	AW971819.1	EST_HUMAN	EST383908 IMAGE resequencing, MAGL Homo sapiens cDNA
2430	7534	12787	3.2	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
115	5317	10459	3.02	4.0E-38	Z25486.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
115	5317	10459	3.02	4.0E-38	Z25486.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1159	6285	11460	0.68	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2091	7206		2.18	3.0E-38	AF035330.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3673	8812		1.76	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnaj-like) (HIRP4), mRNA
3834	8970	14125	1.48	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3834	8970	14126	1.48	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
49	5261	10388	1.51	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1390	6518	11698	6.25	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1658	6786	11980	1.88	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1658	6786	11981	1.88	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
3520	8681		1.04	2.0E-38	AF070670.1	NT	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
4554	9072	14814	14.59	2.0E-38	4557887	NT	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds
1094	6232		1.83	1.0E-38	AA401570.1	EST_HUMAN	Homo sapiens keratin 18 (KRT18) mRNA
2000	7117	12353	1.95	1.0E-38	4885288	NT	zw62b02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element MER19 repetitive element ;
							Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA

Page 95 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2016	7132	12369	1.02	1.0E-38	7661969	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2466	7570	12824	3.73	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4127	9255	14394	1.03	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4301	9423	14550	1.44	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4301	9423	14557	1.44	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4570	9688	14828	1.07	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
53	5265	10392	3.67	8.0E-39	4502312	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1401	6529	11708	1.7	8.0E-39	4758229	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1843	6964		1.95	8.0E-39	AI623404.1	EST_HUMAN	wh53f10.x1 NCI_CGAP_Ki611 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890
2085	7201	12445	3.54	7.0E-39	AL163227.2	NT	POL PROTEIN ;
1008	6152	11319	2.47	5.0E-39	AF003528.1	NT	Homo sapiens chromosome 21 segment HS21C027
2954	8108	13272	6.6	5.0E-39	AI750154.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
549	5714	10848	29.6	4.0E-39	AB015910.1	NT	at36b04.x1 Barstead cdon HPLR57 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
3559	8700	13860	0.71	4.0E-39	AL163210.2	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT : contains LTR7.t1 LTR7 repetitive element ;
46	5258	10380	12.67	3.0E-39	AA631949.1	EST_HUMAN	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
46	5258	10381	12.67	3.0E-39	AA631949.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
46	5258	10382	12.67	3.0E-39	AA631949.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
898	6048		7.83	2.0E-39	BE409203.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
913	6063		11.41	2.0E-39	AI525119.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
1033	6174		3.5	2.0E-39	AF000573.1	NT	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
1644	6672		60.74	2.0E-39	AW372318.1	EST_HUMAN	promner-7.D01.r bvtumor Homo sapiens cDNA 5'
1975	7092	12322	1.87	2.0E-39	AA720574.1	EST_HUMAN	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
2594	7695	12949	1.06	2.0E-39	AL163248.2	NT	PM0-BT0340-211289-003-402 BT0340 Homo sapiens cDNA
4382	9503	14646	1.98	2.0E-39	BF370207.1	EST_HUMAN	PM0-BT0340-211289-003-402 BT0340 Homo sapiens cDNA
1528	6655	11842	2.69	1.0E-39	AJ008345.1	NT	rw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
1528	6655	11843	2.69	1.0E-39	AJ008345.1	NT	THR repetitive element ;
1545	6673	11857	3.43	1.0E-39	7657020	NT	Homo sapiens chromosome 21 segment HS21C048
4630	9748	14893	12.37	1.0E-39	AW951995.1	EST_HUMAN	RC4-FN0037-280700-011-a10 FN0037 Homo sapiens cDNA
4630	9748	14894	12.37	1.0E-39	AW951995.1	EST_HUMAN	Homo sapiens KVLQ11 gene
							Homo sapiens KVLQ11 gene
							Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
							EST364065 IMAGE resequences, MAGB Homo sapiens cDNA
							EST364065 IMAGE resequences, MAGB Homo sapiens cDNA

Page 96 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4671	9787	14932	7.78	1.0E-39	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
554	5719	10851	1.73	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1238	6368	11540	8.31	9.0E-40	4755148	NT	Homo sapiens AE-binding protein 1 (AEBP1), mRNA
1238	6368	11541	8.31	9.0E-40	4755149	NT	Homo sapiens AE-binding protein 1 (AEBP1), mRNA
1462	6589	11778	1.72	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA
3764	8901	14053	0.79	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1), mRNA
3946	10307	14233	3.8	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
3013	8167	13325	0.97	8.0E-40	AA078185.1	EST_HUMAN	7H15A04 Chromosome 7 Hela cDNA Library Homo sapiens cDNA clone 7H15A04
3897	9033		4.43	8.0E-40	BE395541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619168 5'
2689	7786	13035	7.39	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2689	7786	13036	7.39	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2569	7670	12925	1.21	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1887	7007	12227	1.7	4.0E-40	AI686005.1	EST_HUMAN	tt91b01.x1 NCI_CGAP_Py28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR-O73505 O73505 POL PROTEIN.1
2099	7214		2.31	4.0E-40	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4367	9498	14632	8.7	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
4103	9232	14369	0.9	3.0E-40	AI925949.1	EST_HUMAN	wh1207.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
323	5508		5.15	2.0E-40	AI223036.1	EST_HUMAN	qq52h08.x1 Scars_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
795	5949		20.8	2.0E-40	AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW_RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5.1
1838	6959		1.06	2.0E-40	AV731601.1	EST_HUMAN	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1938	7057	12278	4.87	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1938	7057	12279	4.87	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2150	7263	12511	1.99	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
2651	7749		1.89	2.0E-40	BE275932.1	EST_HUMAN	601121567F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
3103	8266	13407	4.43	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
4874	9985	15132	1.41	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4874	9985	15133	1.41	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
884	6034		26.04	1.0E-40	AA225989.1	EST_HUMAN	nc09a09.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
2586	7687	12942	5.11	1.0E-40	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863803 5'
2647	7745		1.35	1.0E-40	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
2659	7795	13045	1.07	1.0E-40	BF541030.1	EST_HUMAN	SYNTAXIN 17 ;
2699	7795	13046	1.07	1.0E-40	BF541030.1	EST_HUMAN	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
3280	8429		1.29	1.0E-40	4507142	NT	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
4582	8700	14838	6.49	1.0E-40	4508012	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
3782	8819	14070	0.6	9.0E-41	W01596.1	EST_HUMAN	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
829	7902	11148	1.72	7.0E-41	A934364.1	EST_HUMAN	zaf36a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294802 5'
829	7902	11149	1.72	7.0E-41	A934364.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
4627	9745	14889	1.16	7.0E-41	BE389592.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
4627	9745	14890	1.16	7.0E-41	BE389592.1	EST_HUMAN	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'
278	5467	10610	2.24	6.0E-41	AB037163.1	NT	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'
2101	7216	12463	1.5	6.0E-41	7657042	NT	Homo sapiens DSCR5b mRNA, complete cds
1814	6937	12153	1.12	5.0E-41	T62628.1	EST_HUMAN	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4083	9212		1.07	5.0E-41	4886636	NT	yc03a10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:78626 3'
389	5558		1.74	4.0E-41	BE156318.1	EST_HUMAN	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
1099	6237	11400	1.26	4.0E-41	AU119344.1	EST_HUMAN	QV0-HT0387-160200-114-09 HT0387 Homo sapiens cDNA
1417	6544	11723	8.1	4.0E-41	A1027117.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
1417	6544	11724	8.1	4.0E-41	A1027117.1	EST_HUMAN	ow45606.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to
1432	6559	11742	1.48	4.0E-41	AB008681.1	NT	TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE.; contains LTR5.b1 LTR5 repetitive element;
1646	6774	11966	4.24	4.0E-41	A1500406.1	EST_HUMAN	ow45606.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to
2856	8010	13171	3.4	4.0E-41	AJ229041.1	NT	TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE.; contains LTR5.b1 LTR5 repetitive element;
2855	8010	13172	3.4	4.0E-41	AJ229041.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
4115	9243	14379	1.67	4.0E-41	X92685.1	NT	tm96c04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1
948	6096	11264	1.53	3.0E-41	AB030176.1	NT	OFR repetitive element ;
4311	9433	14568	2.53	3.0E-41	AB026898.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
							Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
							H. sapiens DNase I hypersensitive site (HSS-3) enhancer element
							Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5090	10190		1.14	3.0E-41	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1837	6704	11894	30.23	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1962	7079	12303	1.48	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end
2201	7313	12585	2.68	2.0E-41	D86962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2248	7358	12615	6.13	2.0E-41	X86631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2788	6704	11894	12.58	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3815	8952	14100	0.81	2.0E-41	5032108	NT	Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA
4691	9709	14847	1.07	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4591	9709	14848	1.07	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
3190	8341	13503	1.06	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
3190	8341	13504	1.06	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4539	9657	14801	12.01	1.0E-41	5678468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
462	5630	10769	4.87	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
5131	10231	15368	0.67	8.0E-42	6679031	NT	Mus musculus neural precursor cell expressed, developmentally down-regulated gene 1 (Nedd1), mRNA
933	6081		2.25	7.0E-42	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C085
1867	6987	12209	2.26	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pikK230) mRNA, complete cds
1867	6987	12210	2.26	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pikK230) mRNA, complete cds
2298	7378		1.62	6.0E-42	AW238656.1	EST_HUMAN	xp29f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1, L1 repetitive element;
4991	10097		1.61	6.0E-42	AI284770.1	EST_HUMAN	qu24h09.x1 NCI_CGAP_Br12 Homo sapiens cDNA clone IMAGE:1965761 similar to contains Alu repetitive element;
131	5329		5.3	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
437	5608	10750	1.3	5.0E-42	BE217913.1	EST_HUMAN	h31e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
486	5654		4.28	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
487	5655		2.43	6.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
752	5908	11064	2.41	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
752	5908	11065	2.41	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
1087	6207	11370	2.48	4.0E-42	AF180111.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4196	9292	14430	1.58	4.0E-42	X59417.1	NT	H.sapiens PROS-27 mRNA
4205	9330	14463	0.97	4.0E-42	AF249219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4227	9352	14485	4.48	4.0E-42	4508468	NT	Homo sapiens regulatory factor X_4 (influences HLA class II expression) (RFX4) mRNA
4557	9675	14815	11.81	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
1493	8620	11810	1.94	2.0E-42	BF376834.1	EST_HUMAN	RCO-TN007B-110800-024-g07 TN007B Homo sapiens cDNA



Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2389	7495		2.16	2.0E-42	AW989344.1	EST_HUMAN	RC3-NN0070-270400-011-110 NN0070 Homo sapiens cDNA
2402	7508	12757	13.69	2.0E-42	AW250069.1	EST_HUMAN	2819293.3 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'
732	5987	11039	2.53	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1044	6185	11352	0.99	1.0E-42	AW295609.1	EST_HUMAN	U1-HB1-af-e-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1102	6240	11403	1.05	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1102	6240	11404	1.05	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1246	7912	11654	10.38	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1246	7912	11555	10.38	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1715	6842	12045	0.95	1.0E-42	11423219	NT	Homo sapiens rec (LOC57201), mRNA
2025	7142	12382	1.17	1.0E-42	AF110298.1	NT	Homo sapiens PDNRP1 gene, exon 17
2616	7619	12867	1.01	1.0E-42	6174468	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2933	8087	13254	5.86	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3666	8825	13980	2.3	1.0E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3772	8909	14062	0.93	1.0E-42	5031610	NT	Homo sapiens Golgi vesicular membrane trafficking protein p18 (BET1) mRNA
3900	9036	14165	1.09	1.0E-42	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4225	9350	14183	1.87	1.0E-42	AL163260.2	NT	Homo sapiens chromosome 21 segment HS21C080
4566	9684	14823	0.99	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161099-012-a03 S.T0197 Homo sapiens cDNA
4711	9827	14970	2.01	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4711	9827	14971	2.01	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4746	9859	15008	4.99	1.0E-42	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4842	9954	15099	1.01	1.0E-42	AB033114.1	NT	Homo sapiens mRNA for KIAA1288 protein, partial cds
651	5812	10947	18.09	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
651	5812	10948	18.09	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
698	5855	11000	5.14	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
698	5855	11001	5.14	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
698	5855	11002	5.14	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
3619	6758	13914	6.42	7.0E-43	AW246442.1	EST_HUMAN	2822251.5 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
1349	6478		32.87	6.0E-43	AA491890.1	EST_HUMAN	nt72d06.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909803 similar to gb:LC50595 60S
2554	7657		2.04	6.0E-43	AV708201.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN);
138	6335		1.73	6.0E-43	AL163213.2	NT	AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'
							Homo sapiens chromosome 21 segment HS21C013

Page 100 of 214  
Table 4  
Single Exon Probes Expressed in BT 474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
502	5669	10803	2.55	5.0E-43	AA382780.1	EST_HUMAN	EST96033 Testis 1 Homo sapiens cDNA 5' end
2809	7965	13126	1.81	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANCO8 5'
974	7867	11290	12.54	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1218	6348		3.61	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1708	6836	12037	4.39	3.0E-43	X67869.1	NT	H. sapiens gene encoding La autoantigen
3558	8699	13859	1.14	3.0E-43	S69002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4266	8391	14529	0.77	3.0E-43	AA548154.1	EST_HUMAN	nk65d06 at NCI_CGAP_P7 Homo sapiens cDNA clone IMAGE:1017419
179	5373		9.84	2.0E-43	AI190764.1	EST_HUMAN	q061c09.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.13 PTR7 PTR7 repetitive element
1662	6790	11985	2.83	1.0E-43	AF154836.1	NT	Homo sapiens Rac-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1682	6790	11986	2.83	1.0E-43	AF154836.1	NT	Homo sapiens Rac-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1720	6847	12051	1.05	1.0E-43	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2886	7783	13031	5.01	1.0E-43	BF348283.1	EST_HUMAN	602022313F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157666 5'
891	6041	11212	4.32	8.0E-44	AI222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
891	6041	11213	4.32	8.0E-44	AI222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
4843	9955	15100	1.08	8.0E-44	AW373185.1	EST_HUMAN	RC5-BT0503-081299-011-g12 BT0503 Homo sapiens cDNA
4843	9955	15101	1.08	8.0E-44	AW373185.1	EST_HUMAN	RC5-BT0503-081299-011-g12 BT0503 Homo sapiens cDNA
658	5819		1.87	7.0E-44	R08035.1	EST_HUMAN	ye89e01.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:124920 5'
2215	7327	12579	1.12	7.0E-44	5031896	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2935	8089	13255	2.28	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2935	8089	13256	2.28	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3841	8977	14132	2.47	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4220	9345	14476	0.99	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4220	9345	14477	0.99	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
5107	10208	15345	0.81	7.0E-44	AF111168.2	NT	Homo sapiens chromosome 21 unknown mRNA
301	5489		3.01	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
330	5513		2.52	5.0E-44	AJ289880.1	NT	Homo sapiens serine palmitoyl transferase, subunit II, gene, complete cds; and unknown genes
3396	8540	13699	3.05	4.0E-44	AL163303.2	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
5002	10107		1.11	4.0E-44	AI435225.1	EST_HUMAN	tt11d02.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
1796	6921		1.25	3.0E-44	6912477	NT	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA
2503	7606	12866	2.91	3.0E-44	BE880628.1	EST_HUMAN	601491529F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893839 5'

Page 101 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3071	8224	13375	5.79	3.0E-44	AA169851.1	EST_HUMAN	zp18605.r1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5'
3867	9003	14161	1.29	3.0E-44	AA337234.1	EST_HUMAN	EST42299 Endometrial tumor Homo sapiens cDNA 5' end similar to similar to alpha-1-antitrypsinase F
1051	6192	11356	2.96	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1051	6192	11357	2.96	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1210	6342	11512	5.87	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1210	6342	11513	5.87	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1316	6445	11624	4.06	2.0E-44	AF133588.1	NT	Homo sapiens RAB38 (RAB38) mRNA, complete cds
1378	6606	11687	1.42	2.0E-44	BE465325.1	EST_HUMAN	hw14g06.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182938 3' similar to SW:OXYB_HUMAN
2136	7250	12490	4.42	2.0E-44	AF070051.1	NT	P22059 OXYSTEROL-BINDING PROTEIN ;
2574	7674		5.92	2.0E-44	5901933	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
3452	8594	13758	1.59	2.0E-44	D87675.1	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
4542	9680	14803	1.43	2.0E-44	AW864379.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
51	5263	10389	8.45	1.0E-44	7657334	NT	PM4-SN0016-120500-003-004 SN0016 Homo sapiens cDNA
51	5263	10390	8.45	1.0E-44	7657334	NT	Homo sapiens MisshepervNIK-related kinase (MINK), mRNA
578	5741	10869	2.85	1.0E-44	AW853132.1	EST_HUMAN	Homo sapiens RC1-CT0249-030300-026-t12 CT0249 Homo sapiens cDNA
1200	6333		1.5	1.0E-44	AW994803.1	EST_HUMAN	RC1-BN0039-110300-012-501 BN0039 Homo sapiens cDNA
1586	6715		5.07	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2206	7318	12568	2.63	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Scores: total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.k3 THR repetitive element ;
2206	7318	12569	2.63	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Scores: total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.k3 THR repetitive element ;
2722	7817	13073	1.32	1.0E-44	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, TS4 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
3706	8844		4.58	1.0E-44	AA455869.1	EST_HUMAN	ae01c09.s1 Scores: NihHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
5095	10195	15333	0.9	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5095	10195	15334	0.9	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
4551	9659	14811	1.96	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379, mRNA
4551	9659	14812	1.96	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
2496	7600	12848	6.36	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5066	10168	15302	7.57	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
2925	8079		1.04	7.0E-45	AL160131.1	NT	Novel human gene mapping to chromosome 22

Page 102 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3951	9086		6.84	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW:R13A_HUMAN P40729 60S RIBOSOMAL PROTEIN L13A;
893	6043		2.58	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2003	7120	12356	2.29	5.0E-45	BF333627.1	EST_HUMAN	GM4-CN0044-180200-515-701 CN0044 Homo sapiens cDNA
3194	8345	13509	2.36	5.0E-45	AI523766.1	EST_HUMAN	tg94f07.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE
1145	6281	11445	8.31	4.0E-45	X95826.1	NT	H. sapiens ART4 gene
2288	7378	12827	3.55	4.0E-45	BE285622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 6'
3312	8459		1.03	3.0E-45	T71480.1	EST_HUMAN	y435f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
4084	8459		1.3	3.0E-45	T71480.1	EST_HUMAN	y435f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
2472	7576		1.46	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3004	8158	13315	1.89	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
119	5576		1.71	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
408	5576		2.76	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
472	5639	10781	1.14	1.0E-46	4509412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1176	6311	11479	1.44	1.0E-45	7657280	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3078	8232	13383	6.31	1.0E-45	U32169.1	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
3473	8615	13782	0.87	1.0E-45	8659558	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
3560	8701	13861	0.72	1.0E-45	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
4456	9575	14714	4.73	1.0E-45	BE396633.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5'
2419	7524	12776	25.33	8.0E-46	AI433201.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5'
2419	7524	12777	25.33	8.0E-46	AI433201.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
2220	7332	12585	1.91	7.0E-46	U46007.1	NT	Rattus norvegicus espin mRNA, complete cds
4553	8671		6.81	7.0E-46	BE386165.1	EST_HUMAN	601277262F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
4775	9888		1.48	7.0E-46	BE064386.1	EST_HUMAN	RC4-BT0310-110300-016-F10 BT0310 Homo sapiens cDNA
2718	7813	13068	3.3	6.0E-46	AI894361.1	EST_HUMAN	wm3108.x1 NCI CGAP U4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
2718	7813	13069	3.3	6.0E-46	AI894361.1	EST_HUMAN	WM3108.x1 NCI CGAP U4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
201	5398		5.07	5.0E-46	AL163210.2	NT	MER19 repetitive element;
3515	8656	13822	1.28	5.0E-46	BE677194.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3515	8656	13823	1.28	5.0E-46	BE677194.1	EST_HUMAN	7481g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
							7481g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'

Page 103 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
640	5801		1.91	4.0E-46	AA601143.1	EST_HUMAN	ns54e09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_mn1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1719	6846	12049	8.22	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_mn1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
1719	6846	12050	8.22	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_mn1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
2702	7798	13049	1.41	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
5125	10226	15361	0.65	4.0E-46	BE044280.1	EST_HUMAN	h042a07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040020 3'
5125	10226	15362	0.65	4.0E-46	BE044280.1	EST_HUMAN	h042a07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040020 3'
2141	7255	12501	2.26	3.0E-46	5453620	NT	Homo sapiens solute carrier family 35 (CNP-sialic acid transporter), member 1 (SLC35A1), mRNA
2262	7372	12626	1.87	3.0E-46	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA
2406	7512	12762	7.52	3.0E-46	AF160212.1	NT	Homo sapiens VAMP-associated 33 kDa protein mRNA, complete cds
4371	9492	14636	0.81	3.0E-46	4508376	NT	Homo sapiens mitogen-activated protein kinase kinase 3 (MAP4K3), mRNA
4742	9855	15002	1.38	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
4742	9855	15003	1.38	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
838	5990	11158	8.59	2.0E-46	AA468948.1	EST_HUMAN	ne06a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;
1577	5706		1.15	2.0E-46	AA678246.1	EST_HUMAN	z127a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431986 3'
1652	6780	11972	2.96	2.0E-46	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
4959	10067	15204	1.07	2.0E-46	AA398286.1	EST_HUMAN	z159e02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE Q01730 RSP-1 PROTEIN.;
1236	6366	11539	4.96	1.0E-46	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2258	7368	12624	2.78	1.0E-46	AW978516.1	EST_HUMAN	EST390625 IMAGE resequences, MAGP Homo sapiens cDNA
2377	7483	12737	2.35	1.0E-46	H97330.1	EST_HUMAN	EST480095 WATM1 Homo sapiens cDNA clone 480095
3232	8382	13542	1.72	1.0E-46	AA631912.1	EST_HUMAN	np78602.s1 NCI_CGAP_P2 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens MT-11 mRNA, (HUMAN);
4844	9856		3.11	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
766	5920		3.32	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudocautosomal region; segment 1/2

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4910	10020	15165	3.19	9.0E-47	AW770928.1	EST_HUMAN	h193e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703
1820	6943	12161	11.91	8.0E-47	Y18536.1	NT	HYPOTHETICAL 12.4 KD PROTEIN. ;
1820	6943	12162	11.91	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
							Homo sapiens HLA-C gene, exon 5, individual 19323
2678	7775	13026	1.41	8.0E-47	5453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
2998	8151	13312	1.6	8.0E-47	AJ229043.1	NT	Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22, segment 3/3
3606	8745	13900	0.75	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
3606	8745	13901	0.75	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
2519	7623	12869	1.27	6.0E-47	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
1407	6534	11713	3.52	4.0E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
543	5709	10844	6.99	3.0E-47	BE007634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
543	6709	10845	6.99	3.0E-47	BE007634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
819	5972	11134	3.04	3.0E-47	N57483.1	EST_HUMAN	y54b04.s1 Soares multiple sclerosis 2NBHMSF Homo sapiens cDNA clone IMAGE:277927 3'
945	6093	11261	7.87	3.0E-47	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2023	7140	12380	4.73	3.0E-47	AB007869.1	NT	Homo sapiens KIAA0439 mRNA, partial cds
3285	8434	13596	0.76	3.0E-47	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3639	9075		4.78	3.0E-47	U93181.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SDF1) mRNA, partial cds
4340	9462	14589	1.32	3.0E-47	M12959.1	NT	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
143	5340	10484	1.27	2.0E-47	4505318	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
969	6116	11284	2.44	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
969	6116	11285	2.44	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1606	6734	11627	3.51	2.0E-47	7662109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
1691	6820	12019	3.36	2.0E-47	AA524514.1	EST_HUMAN	ng43h12.s1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:937607 3'
4324	9446	14579	1.79	2.0E-47	4504868	NT	Homo sapiens ring finger protein (C3HC4 type) B (RNF8), mRNA
4363	9485	14626	1.64	2.0E-47	AA569592.1	EST_HUMAN	m23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4363	9485	14627	1.64	2.0E-47	AA569592.1	EST_HUMAN	m23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4483	9602	14741	1.72	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4781	9804	15040	1.14	2.0E-47	AW965186.1	EST_HUMAN	EST377239 MAGIE resequences, MAG1 Homo sapiens cDNA
5181	10278	15416	1.01	2.0E-47	9055268	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDT), mRNA
1413	6540	11717	4.29	1.0E-47	A1333429.1	EST_HUMAN	qp99h03.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3'
3800	8937	14083	0.98	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3800	8937	14084	0.98	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5059	10161	16294	2.53	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA

Page 105 of 214  
Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1625	6753	11946	2.36	9.0E-48	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CAQNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1254	6384		1.3	8.0E-48	4501600	NT	Homo sapiens aminocyclase 1 (ACY1), mRNA
1255	6384		1.17	8.0E-48	4501600	NT	Homo sapiens aminocyclase 1 (ACY1), mRNA
3113	8266	13421	3.72	8.0E-48	AW768477.1	EST_HUMAN	hK61b03.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
3113	8266	13422	3.72	8.0E-48	AW768477.1	EST_HUMAN	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
490	5658		1.47	7.0E-48	AB033035.1	NT	hK61b03.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
491	5658		12.54	7.0E-48	AB033035.1	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
1511	6638	11825	1.42	7.0E-48	8912719	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1648	6776	11968	5.89	7.0E-48	5730038	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
3584	8725	13883	0.93	6.0E-48	A176111.1	EST_HUMAN	Homo sapiens taurin-like kinase 1 (TLK1), mRNA
3281	10305	13600	1.62	5.0E-48	4828891	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1978	7095	12325	35.4	3.0E-48	4885170	NT	wic6903.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398613 3'
1978	7095	12326	35.4	3.0E-48	4885170	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
3611	8750	13907	0.7	3.0E-48	AW684531.1	EST_HUMAN	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
44	5256	10377	2.62	2.0E-48	AA631940.1	EST_HUMAN	h14b12.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCRB_HUMAN
4506	9625	14768	1.11	2.0E-48	BE246065.1	EST_HUMAN	P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
5199	10296	15433	0.97	2.0E-48	X57147.1	NT	fric7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26
55	5266	10394	11.65	1.0E-48	7706534	NT	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842
874	6025	11196	8.27	1.0E-48	4502166	NT	Human endogenous retrovirus pHE.1 (ERV9)
1077	6217	11381	2.48	1.0E-48	7657430	NT	Homo sapiens dispirin resistance-associated overexpressed protein (LOC51747), mRNA
1077	6217	11382	2.48	1.0E-48	7657430	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1300	6430	11604	4.11	1.0E-48	5032032	NT	Homo sapiens EBNA-2 co-activator (100Kd) (p100), mRNA
1921	7040	12281	39.39	1.0E-48	AL163302.2	NT	Homo sapiens EBNA-2 co-activator (100Kd) (p100), mRNA
3468	8611	13777	0.91	1.0E-48	AL163246.2	NT	Homo sapiens RNA binding motif protein 8 (RBM8) mRNA
5113	10214	15351	1.22	1.0E-48	M10976.1	NT	Homo sapiens chromosome 21 segment HS21C102
2007	7124	12360	1.23	8.0E-49	AB026497.1	NT	Homo sapiens chromosome 21 segment HS21C048
135	5561	10704	2.55	7.0E-49	5729990	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
135	5561	10705	2.55	7.0E-49	5729990	NT	Mus musculus MyoPDZ mRNA for myosin containing PDZ domain, complete cds
135	5561	10705	2.55	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
135	5561	10705	2.55	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA

Page 106 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
392	5561	10704	1.56	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
392	5561	10705	1.56	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	5561	10704	2.3	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	5561	10705	2.3	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1223	6355	11525	4.13	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
194	5389	10532	71.58	6.0E-49	AW731740.1	EST_HUMAN	ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:X17206.40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
1365	6494	11675	1.28	6.0E-49	BF038269.1	EST_HUMAN	601457738F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3861272 5'
1365	6494	11678	1.26	6.0E-49	BF038269.1	EST_HUMAN	601457738F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3861272 5'
710	5867	11013	7.34	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
710	5867	11014	7.34	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1806	6930	12145	2.24	5.0E-49	AA172121.1	EST_HUMAN	zp26c07.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G233228 G233228 RTVL-H PROTEIN; contains LTR7.19 LTR7 LTR7 repetitive element;
2713	7808	13062	7.74	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
3256	8406	13567	8.36	5.0E-49	11438355	NT	Homo sapiens similar to ribosomal protein S27 (metalloprotein 1) (H. sapiens) (LOC63362), mRNA
523	5689	10820	23.9	4.0E-49	AW189533.1	EST_HUMAN	xi08501.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP.B0350.2B CE08703;
559	5724	10555	3.83	3.0E-49	X68968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element;
2609	7708		1.11	3.0E-49	AA016131.1	EST_HUMAN	Human type IV collagen (COL4A6) gene, exon 40
4968	10076	15214	2.28	3.0E-49	U46993.1	NT	MR3-HT0487-150200-119-g01 HT0487 Homo sapiens cDNA
660	5821		1.55	2.0E-49	BE165980.1	EST_HUMAN	yr23406.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:262571 5'
3207	8358	13519	1.73	2.0E-49	N26446.1	EST_HUMAN	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
3556	8697	13857	0.65	2.0E-49	AF026584.1	NT	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
900	6050		9.92	1.0E-49	BF033327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1568	6696	11863	30.86	1.0E-49	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1813	6938	12152	3.89	1.0E-49	BE255216.1	EST_HUMAN	60115768F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 5'
4980	10088		1.57	9.0E-50	AF101475.1	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
165	5361	10501	3.43	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
717	5874	11021	1.6	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
717	5874	11022	1.6	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2



Page 107 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1034	6175		1.65	8.0E-50	AF000573.1	NT	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds
1774	6900	12108	3.81	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2455	7559	12810	1.91	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2455	7559	12811	1.91	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2660	7758	13007	3.04	8.0E-50	4826658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
616	5776	10907	2.59	7.0E-50	BE089591.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
5191	10288	15424	0.92	7.0E-50	BE087807.1	EST_HUMAN	QV1-BT0681-260400-181-g02 BT0681 Homo sapiens cDNA
5191	10288	15425	0.92	7.0E-50	BE087807.1	EST_HUMAN	QV1-BT0681-260400-181-g02 BT0681 Homo sapiens cDNA
4320	9442		0.73	6.0E-50	BE794381.1	EST_HUMAN	601589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
1805	6929	12143	1.36	6.0E-50	BF332938.1	EST_HUMAN	CNM0-BT0792-300500-388-b05 BT0792 Homo sapiens cDNA
1805	6929	12144	1.36	5.0E-50	BF332938.1	EST_HUMAN	CNM0-BT0792-300500-388-b05 BT0792 Homo sapiens cDNA
917	6066		2.42	4.0E-50	AA601143.1	EST_HUMAN	ncs4e09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1
9430	8572	13732	0.96	4.0E-50	AL163248.2	NT	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1842	7061		2.01	3.0E-50	M18048.1	NT	Homo sapiens chromosome 21 segment HS21C048
2489	7593	12841	1.4	3.0E-50	BE259198.1	EST_HUMAN	601103717F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350309 5'
3281	8430	13592	0.63	3.0E-50	AA746142.1	EST_HUMAN	cb03f06.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322827 3'
778	5932		5.43	2.0E-50	AF055068.1	NT	Homo sapiens MHC class 1 region
1081	6220	11386	5.34	2.0E-50	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
1454	6581	11770	1.39	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
3271	8420	13581	1.06	2.0E-50	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes
4234	9359	14491	0.66	2.0E-50	D86424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
4849	9961	15105	1.16	2.0E-50	AW866159.1	EST_HUMAN	MR3-SN0066-040500-008-401 SN0066 Homo sapiens cDNA
4849	9961	15106	1.16	2.0E-50	AW866159.1	EST_HUMAN	MR3-SN0066-040500-008-401 SN0066 Homo sapiens cDNA
461	5629	10768	1.82	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2345	7452		4.95	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4540	9658	14802	8.31	8.0E-51	AA610842.1	EST_HUMAN	np88e09.s1 NCI_CGAP_Lut1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_ma1
2988	8143	13305	0.7	7.0E-51	AW274720.1	EST_HUMAN	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
3266	8415	13577	1.42	7.0E-51	AW869219.1	EST_HUMAN	xn34a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340
3344	8490	13656	0.7	7.0E-51	AW274720.1	EST_HUMAN	QV4-NT0028-200400-180-405 NT0028 Homo sapiens cDNA
4138	9266	14405	1.01	7.0E-51	AL079628.1	EST_HUMAN	xn34a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340
							Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
							DKFZp434B2229.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'

Page 108 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4138	8268	14406	1.01	7.0E-51	AL079628.1	EST_HUMAN	DKFZp434B2229.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4328	9450	14583	1.33	7.0E-51	AW285603.1	EST_HUMAN	UI-H-BWO-aip-b-05-0-UI s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729817 3'
1542	6670	11856	1.02	6.0E-51	6678763	NT	Homo sapiens putative DNA binding protein (M86), mRNA
1981	7098	12329	3.03	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3455	8597	13761	13.36	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
792	5946	11106	6.93	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
804	5957	11120	1.73	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
992	7906	11307	1.05	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1621	6749	11943	2.16	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2555	7658	12809	5	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoporin 155
3016	9052	14211	1.63	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3916	9052	14212	1.63	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5054	10158	15287	1.44	5.0E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
130	5328	10474	57.38	3.0E-51	AI587348.1	EST_HUMAN	tr81c09.x1 NCL_CGAP_Par1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1178	6313	11481	185.78	3.0E-51	AI587348.1	EST_HUMAN	tr81c09.x1 NCL_CGAP_Par1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4303	9425	14560	1.99	3.0E-51	AL159142.1	NT	Novel human gene mapping to chromosome 22
364	5544	10886	5.18	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
686	5844	10983	2.35	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
686	5844	10984	2.35	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1702	6830	12032	4.18	2.0E-51	AA233352.1	EST_HUMAN	z30a05.r1 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:G233228 G233228 RTVL-H PROTEIN, contains LTR7.0 LTR7 repetitive element;
3714	8852	14006	2.49	2.0E-51	AA492415.1	EST_HUMAN	427g03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
4489	9588	14727	0.87	2.0E-51	AW137828.1	EST_HUMAN	UI-H-BT1-aq-d-02-0-UI s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'
110	5314	10453	27.83	1.0E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1506	6533		49.08	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBC12 5'
3168	8319	13481	1.41	1.0E-51	AF000994.1	NT	Homo sapiens ubiquitin TPR motif, Y isoform (UTY) mRNA, alternative transcript 3, complete cds
147	5344	10487	8.69	8.0E-52	AA720574.1	EST_HUMAN	hw21g02.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
1510	6637	11824	1.7	8.0E-52	X84900.1	NT	H. sapiens mRNA for laminin-5, alpha3b chain

Page 109 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1667	6795	11990	1.87	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1667	6795	11991	1.87	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3969	6795	11990	6.18	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3969	6795	11991	6.18	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1189	6323		1.38	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271289-049-c07 BT0537 Homo sapiens cDNA
1707	6835	12036	2.13	6.0E-52	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4418	9538	14679	1.7	5.0E-52	Z78888.1	NT	H. sapiens flow-sorted chromosome 9 HindIII fragment, SC00A18H7
1675	6804	11999	1.24	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1708	6923	12133	1.17	4.0E-52	4758843	NT	Homo sapiens nucleoprotein 155kD (NUP155) mRNA
3901	9037	14196	0.77	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4088	9198		10.28	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
561	5728	10856	3.35	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
561	5728	10857	3.35	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1768	6894	12101	1.78	2.0E-52	AB007899.1	NT	Homo sapiens KIAA0439 mRNA, partial cds
2470	7574	12827	4.79	2.0E-52	BE207575.1	EST_HUMAN	b565b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:U16493 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE);
2698	7794		13.92	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248991 5'
4982	10070	15206	4.19	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5000	10105	15235	1.13	2.0E-52	AI141802.1	EST_HUMAN	qa56a05.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5000	10105	15236	1.13	2.0E-52	AI141802.1	EST_HUMAN	qa56a05.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
531	5697	10830	1.3	1.0E-52	AA634445.1	EST_HUMAN	zu75h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
1380	6508	11689	12.29	1.0E-52	4504028	NT	Homo sapiens glutamate-aminomethylase (glutamine synthase) (GLUL) mRNA
2508	7611		1.76	1.0E-52	4502238	NT	Homo sapiens arylsulfoxide D (ARSD), transcript variant 1, mRNA
3031	8185	13340	1.58	1.0E-52	S61070.1	NT	pol=reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]
4370	9491	14635	0.93	9.0E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
5178	10275	15413	1.59	9.0E-53	AB040937.1	NT	Homo sapiens mRNA for KIAA1504 protein, partial cds
4074	9204	14340	7.43	5.0E-53	4758543	NT	Homo sapiens heterotetranucleic nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
48	6260	10384	1.49	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085

Page 110 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
48	5260	10385	1.49	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4789	8902	15043	1.29	4.0E-53	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2621	7720	12974	1.42	3.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3712	8850	14004	0.99	3.0E-53	AW050836.1	EST_HUMAN	wz22cd07.x1 Soares_Diethylstilbestrol-induced human chromosome 11p15.5 gene, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4563	9881	14820	1.22	3.0E-53	AW803563.1	EST_HUMAN	IL2-JM0081-240300-055-D03 JM0081 Homo sapiens cDNA
457	5625		3.25	2.0E-53	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
2308	7417	12687	16.62	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2509	7612		4.96	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA
2688	7785	13033	1.12	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2688	7785	13034	1.12	2.0E-53	4757815	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
4033	9164	14306	3.37	2.0E-53	M61873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
5193	10290	15427	1.4	2.0E-53	7662083	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
1458	6585	11773	2.62	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3391	8535	13698	1.24	1.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4945	10054	15192	1.07	1.0E-53	BE293886.1	EST_HUMAN	601176725F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531919 5'
204	5399	10541	4.55	8.0E-54	BE388785.1	EST_HUMAN	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
1849	6970	12191	1.84	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
382	5591	10736	1.12	7.0E-54	AA812537.1	EST_HUMAN	al79c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element;
1844	6955	12186	1.14	7.0E-54	Y16645.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2
2198	7300	12549	2.51	7.0E-54	N27177.1	EST_HUMAN	yw88d12.s1 Soares_placenta_8to9weeks_2NblHP808W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7.k3 LTR7 repetitive element;
23	5234	10348	1.12	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
383	5592	10737	1.03	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
383	5592	10738	1.03	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3267	8416	13578	0.9	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3979	9113	14261	1.15	6.0E-54	4502872	NT	Homo sapiens chloride channel 8 (CLCN8) mRNA
4441	9560	14702	1.05	6.0E-54	AV754746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPGAAC10 5'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4812	9924	15065	2.14	6.0E-54	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4845	9957		1.47	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p66 isoform
4886	9957		2.77	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p66 isoform
2135	7249	12495	7.96	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
178	5372		261.14	4.0E-54	AF110103.1	NT	Tupala belangeri beta-actin mRNA, partial cds
957	6105	11274	223.4	4.0E-54	AA306764.1	EST_HUMAN	EST177686 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1817	6940	12167	2.25	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1817	6940	12158	2.25	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3187	8339		1.52	4.0E-54	A1935086.1	EST_HUMAN	wd26d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329289 3' similar to TR:002711
89	5298	10437	11.81	3.0E-54	AA313487.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2589	7690		1.02	3.0E-54	A1908757.1	EST_HUMAN	IL-BT188-190398-007 BT188 Homo sapiens cDNA
641	5802	10835	4.73	2.0E-54	5031800	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1374	5502	11684	1.16	2.0E-54	4507164	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
1582	6691	11877	1.14	2.0E-54	AA655008.1	EST_HUMAN	nt78a09.s1 NCJ_CGAP_P13 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element
2511	7614	12864	2.46	2.0E-54	AW163175.1	EST_HUMAN	eu92g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW:CU1.1_HUMAN Q13616 CULLIN HOMOLOG 1;
2584	7665	12920	1.03	2.0E-54	AL163210.2	NT	Homo sapiens chromosome 21 segment HS210010
2861	8016	13182	1.15	2.0E-54	AW057524.1	EST_HUMAN	wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2652927 3' similar to TR:062084 Q62084 PHOSPHOLIPASE C NEIGHBORING;
3535	8677		8.84	2.0E-54	AA532925.1	EST_HUMAN	nt45g09.s1 NCJ_CGAP_P19 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X63777 60S RIBOSOMAL PROTEIN L23 (HUMAN);
3827	8963	14113	0.72	2.0E-54	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
3827	8963	14114	0.72	2.0E-54	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4177	8303		3.15	2.0E-54	4502642	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
4419	9539		0.95	2.0E-54	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4850	9962	15107	1.18	2.0E-54	7708448	NT	Homo sapiens peptidylarginine deiminase type III (LOC51702), mRNA
4444	9563		1.41	1.0E-54	BF315418.1	EST_HUMAN	60189230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128635 5'
1320	9449		0.72	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1323	6452		2.12	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1780	6906	12113	1.39	5.0E-55	AA704971.1	EST_HUMAN	z95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
1780	6906	12114	1.39	5.0E-55	AA704971.1	EST_HUMAN	z95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'

Page 112 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4737	9850	14997	1.57	5.0E-55	AW208021.1	EST_HUMAN	UIH-B11-efy-g-09-0-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723536 3'
54	7882	10393	3.01	4.0E-55	AW957994.1	EST_HUMAN	EST370064 MAGE resequences. MAGE Homo sapiens cDNA
671	8630	10970	31.27	4.0E-55	4926373	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1451	6579	11766	1.54	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1451	6579	11767	1.34	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1529	6656		1.93	4.0E-55	BF061411.1	EST_HUMAN	752b10.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.13 L1 repetitive element
2018	7135	12373	4.48	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2018	7135	12374	4.48	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2078	7194	12437	3.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (DGKG) mRNA
2078	7194	12438	3.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (DGKG) mRNA
2287	7396	12648	7.71	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
3263	8412	13574	1.07	4.0E-55	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
375	5553	10697	2.83	2.0E-55	X57147.1	NT	Human endogenous retrovirus phiE.1 (ERV9)
550	5715		1.74	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
648	5809	10944	3.88	2.0E-55	4507298	NT	Homo sapiens syntaxin-binding protein 1 (STXBP1) mRNA, and translated products
2926	8080	13248	2.08	2.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4741	9854	15001	2.82	2.0E-55	BE719986.1	EST_HUMAN	CM1-HT0876-150800-357-gp3 HT0876 Homo sapiens cDNA
92	5301	10440	1.55	1.0E-55	4505060	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
186	5381	10522	78.12	1.0E-55	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
1151	6287	11452	3.98	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1955	7072	12296	47.44	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
1955	7072	12297	47.44	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
2305	7414		4.47	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2488	7592	12840	9.54	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2524	7627	12873	2.04	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2524	7627	12874	2.04	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2575	7675	12829	3.13	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
3390	8534	13695	0.97	1.0E-55	W28180.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
3964	9099	14246	3.8	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4270	9394	14533	1.19	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4698	9815		1.15	1.0E-55	N77261.1	EST_HUMAN	yw44g03 J1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245620 5'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4796	9909	15049	4.45	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
4798	9909	15050	4.45	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
5112	10213	15350	1.07	1.0E-55	8923126	NT	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA
2695	7792	13042	3.22	7.0E-56	H19934.1	EST_HUMAN	Yn62g03.1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element;
1706	6834	12035	1.43	5.0E-56	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-101 BN0053 Homo sapiens cDNA
26	5237	10351	28.3	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
26	5237	10352	28.3	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2155	7288	13017	1.1	4.0E-56	BF207598.1	EST_HUMAN	601862059F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081551 5'
2670	7766	13017	6.1	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2670	7766	13018	6.1	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2773	5690	10822	5.49	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2793	7679	12933	1.15	4.0E-56	A1632488.1	EST_HUMAN	wb09f08.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA P27119 ORNITHINE DECARBOXYLASE;
2793	7679	12934	1.15	4.0E-56	A1632488.1	EST_HUMAN	wb09f08.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA P27119 ORNITHINE DECARBOXYLASE;
1347	6478	11656	4.09	3.0E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1775	6801	12109	4.35	3.0E-56	6912743	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
2134	7248	12494	1.14	3.0E-56	6912697	NT	Homo sapiens oncogene TC21 (TC21), mRNA
3102	8255	13405	1.85	3.0E-56	AA325628.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3102	8255	13405	1.85	3.0E-56	AA325628.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3812	8949		2.77	3.0E-56	AF055066.1	NT	Homo sapiens MHC class 1 region
3892	9028	14187	0.76	3.0E-56	BE393512.1	EST_HUMAN	601310203F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5'
4402	9522	14693	4	3.0E-56	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
4545	9663	14806	2.31	3.0E-56	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
522	5688		2.42	2.0E-56	AA199818.1	EST_HUMAN	z452a08.s1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645206 3'
731	7899	11037	2.24	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
731	7899	11038	2.24	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2957	8111	13274	1.4	2.0E-56	AB037835.1	NT	Homo sapiens protein for KIAA1414, protein, partial cds
3297	8444		1.86	2.0E-56	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3521	8662	13829	1.11	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
981	6127		3.5	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds

Page 114 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1536	6663	11849	5.72	1.0E-56	AA293036.1	EST_HUMAN	z54b09.1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:726137 5' similar to gb:M94854
3652	8791	13945	1.81	1.0E-56	AW599833.1	EST_HUMAN	INTERLEUKIN ENHANCER-BINDING FACTOR (HUMAN);
3652	8791	13946	1.81	1.0E-56	AW599833.1	EST_HUMAN	hg23ct11.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2946452 3'
5015	10118	15251	1.04	1.0E-56	AI905162.1	EST_HUMAN	hg23ct11.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2946452 3'
624	5784		1.74	9.0E-57	AW880885.1	EST_HUMAN	QV-BT07-130199-079 BT077 Homo sapiens cDNA
295	5483	10625	2.62	8.0E-57	AW816405.1	EST_HUMAN	QV0-OT0033-070300-152-h03 OT0033 Homo sapiens cDNA
895	6035	11206	7.79	8.0E-57	AW264599.1	EST_HUMAN	QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA
1828	6951	12173	1.46	8.0E-57	AA498109.1	EST_HUMAN	xf05d10.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U06875
2598	7698	12962	6.47	7.0E-57	7657592	NT	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
2598	7698	12963	6.47	7.0E-57	7657592	NT	z561b12.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:767151 5'
3233	8383	13543	1.26	7.0E-57	7242168	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3233	8383	13544	1.26	7.0E-57	7242168	NT	Homo sapiens NME7 (NME7), mRNA
3254	8404	13566	0.78	7.0E-57	6005979	NT	Homo sapiens NME7 (NME7), mRNA
3855	8991	14147	1.61	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3855	8991	14148	1.61	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3734	8872	14024	2.03	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4990	10096	15227	1.05	4.0E-57	BE783649.1	EST_HUMAN	601471238F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874135 5'
805	5958	11121	2.34	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1336	6464		51.92	3.0E-57	AA230270.1	EST_HUMAN	nc1307.s1 NCI_CGAP_P71 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2388	7474	12728	1.39	3.0E-57	AA348335.1	EST_HUMAN	P46783 40S RIBOSOMAL PROTEIN S10. ;
2664	7760	13011	1.49	3.0E-57	BE676622.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' end
2664	7760	13012	1.49	3.0E-57	BE676622.1	EST_HUMAN	733b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2
3674	8913		80.77	3.0E-57	AW953064.1	EST_HUMAN	CE20263 ;
4037	9188	14309	5.42	3.0E-57	P08547	SWISSPROT	RC3-CT0254-110300-027-d10 CT0254 Homo sapiens cDNA
1443	6571	11758	1.17	2.0E-57	A1478904.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1515	6642	11828	1.6	2.0E-57	AF246219.1	NT	Im25c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157618 3' similar to contains Alu repetitive element.
							Homo sapiens SNARE protein kinase SNAK mRNA, complete cds



Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST-E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1515	6842	11829	1.8	2.0E-57	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
2378	7484	12738	0.97	2.0E-57	BE172628.1	EST_HUMAN	MRO-HT0559-010400-009-h10 HT0559 Homo sapiens cDNA
2691	7788	13038	2.49	2.0E-57	AA845419.1	EST_HUMAN	ak02502.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
3420	8562		1.38	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3538	8680	13842	0.7	2.0E-57	R07702.1	EST_HUMAN	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3538	8680	13843	0.7	2.0E-57	R07702.1	EST_HUMAN	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3904	9040	14200	1.15	2.0E-57	BE073264.1	EST_HUMAN	MRO-BT0551-060300-103-b03 BT0551 Homo sapiens cDNA
4485	9804	14742	6.05	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2213	7325	12575	1.07	1.0E-57	AW503208.1	EST_HUMAN	UI-HF-BND-ekt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
587	5749		15.12	8.0E-58	BE868715.1	EST_HUMAN	607445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
653	5814	10950	4.07	8.0E-58	AI798376.1	EST_HUMAN	t34507.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN;
653	5814	10951	4.07	8.0E-58	AI798376.1	EST_HUMAN	t34507.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN;
1868	6988	12211	1.51	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1868	6988	12212	1.51	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2944	8098		2.52	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
4900	10011	15158	1.53	7.0E-58	BE206903.1	EST_HUMAN	ba05g04.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823510 5' similar to TR:Q61489 Q61489 DHM1 PROTEIN;
2234	7346	12601	1.02	6.0E-58	BE395061.1	EST_HUMAN	607309495F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2355	7482	12718	8	6.0E-58	AU130680.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
2868	8020	13186	0.98	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
2868	8020	13187	0.98	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
298	5485	10627	3.03	5.0E-58	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
708	5865	11012	5.2	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160600-016-b05 NT0057 Homo sapiens cDNA
1197	6331	11499	3.29	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1197	6331	11500	3.29	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1198	6331	11499	2.28	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1198	6331	11500	2.28	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3304	8451	13613	3.85	6.0E-58	AA988183.1	EST_HUMAN	or98e07.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603808 3'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4232	8357	14489	0.67	5.0E-58	AI636745.1	EST_HUMAN	ts89e07.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2238468 3' similar to SW:PRO2_ACACA P19984 PROFILIN II;
371	5551	10694	5.7	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5C) mRNA
797	5951	11111	1.23	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
1480	6607	11793	0.99	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2541	7844	12894	1.03	4.0E-58	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
2596	7697	12950	2.03	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3306	8453	13615	1	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3721	8859	14012	1.02	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
333	5516		2.93	3.0E-58	R17879.1	EST_HUMAN	yg10902.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
1386	6524	11703	1.81	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
3158	8309	13488	3.32	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
3158	8309	13489	3.32	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
940	6088	11256	8.84	2.0E-58	AF068624.1	NT	Homo sapiens 5-aminolevulinic acid synthase 2 (ALAS2) gene, complete cds
							bc08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X68391 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
1294	6423		39.27	2.0E-58	BE208532.1	EST_HUMAN	
720	5877	11024	0.65	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3' end
1069	6209	11372	5.86	1.0E-58	6274349	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1332	6461	11640	3.63	1.0E-58	AW957182.1	EST_HUMAN	EST389252 MAGC resequences, MAGD Homo sapiens cDNA
1332	6461	11641	3.63	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGC resequences, MAGD Homo sapiens cDNA
1877	6806	12003	1.29	1.0E-58	BE466132.1	EST_HUMAN	hy10f08.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:3196935 3'
2763	7857	13113	2.83	1.0E-58	4759169	NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA
2791	7125	12361	1.49	1.0E-58	5174444	NT	Homo sapiens G protein-coupled receptor 69A (GPR69A) mRNA
3700	8838	13992	0.77	1.0E-58	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNF1) mRNA
4955	10063	15202	4.97	1.0E-58	A1141063.1	EST_HUMAN	oz43h01.x1 Soares_NhiHMFu_S1 Homo sapiens cDNA clone IMAGE:1678129 3'
2211	7323	12573	46.86	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
173	7884		2.08	6.0E-59	BF036327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
							au83h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:075786 075786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
1765	6891	12097	0.96	5.0E-59	AW157281.1	EST_HUMAN	

Page 117 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1765	6891	12098	0.98	5.0E-59	AW157281.1	EST_HUMAN	au93h05.x1 Schneider field brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to
3104	8257	13408	6.48	5.0E-59	A1807484.1	EST_HUMAN	TR-O75786 075786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.
4628	9746	14881	7.69	5.0E-59	X83497.1	NT	W48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
794	5948	11109	2.42	4.0E-59	D80006.1	NT	H.sapiens DNA for ZNF80-linked ERV9 long terminal repeat
1241	6371	11545	5.89	4.0E-59	4505818	NT	Human mRNA for KIAA0784 gene, partial cds
1241	6371	11545	5.89	4.0E-59	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
5184	10262	15401	1.74	4.0E-59	A1990847.1	EST_HUMAN	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
9	5220	10554	4.88	3.0E-59	AW065524.1	EST_HUMAN	ws32a12.X1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2498926 3'
224	5417	10554	3.58	3.0E-59	7692247	NT	EST377582 MAGIE resequences, MAGI Homo sapiens cDNA
1725	6852	12056	6.78	3.0E-59	4505860	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1725	6852	12057	6.78	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2120	7235	12477	4.6	3.0E-59	AB029035.1	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2120	7235	12478	4.6	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2732	7950	13082	1.01	3.0E-59	AF232298.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3106	8259	13412	3.82	3.0E-59	4502014	NT	Homo sapiens NF1-2 pseudogene, exon 17
3106	8259	13413	3.82	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3804	8941	14089	1.71	3.0E-59	4508044	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
4689	9775	14921	1.35	3.0E-59	AL163284.2	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4809	9921	15093	1.62	3.0E-59	7427522	NT	Homo sapiens chromosome 21 segment HS21C084
158	5355		15.3	1.0E-59	BE298411.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2592	7683		1.63	1.0E-59	AA748468.1	EST_HUMAN	60176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
793	5918	11075	2.32	8.0E-60	AW977845.1	EST_HUMAN	ca56h11.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13537
1493	6610	11796	3.19	8.0E-60	4759159	NT	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.
2162	7265	12513	6.25	8.0E-60	5174656	NT	EST388849 MAGIE resequences, MAGO Homo sapiens cDNA
2162	7265	12514	5.25	8.0E-60	5174656	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
753	5909	11066	4.23	7.0E-60	AF055066.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
754	5909	11066	13.42	7.0E-60	AF055066.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
816	5969	11130	1.08	7.0E-60	4504634	NT	Homo sapiens MHC class 1 region
2119	7294	12476	2.96	7.0E-60	AF077188.1	NT	Homo sapiens MHC class 1 region
2746	7840	13095	1.02	7.0E-60	AB011153.1	NT	Homo sapiens MHC class 1 region
							Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
							Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
							Homo sapiens mRNA for KIAA0581 protein, partial cds

Page 118 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4150	9276	14413	2.53	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
4548	9666	14808	0.84	7.0E-60	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2159	7272	12520	1.47	8.0E-60	BE964974.2	EST_HUMAN	601658751R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886069 3'
80	5289	10428	1.9	5.0E-60	AI807917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
80	5289	10429	1.9	5.0E-60	AI807917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2216	7328	12580	1.14	4.0E-60	AW503208.1	EST_HUMAN	UI-HF-BND-ekt-g-07-0-UI1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2216	7328	12581	1.14	4.0E-60	AW503208.1	EST_HUMAN	UI-HF-BND-ekt-g-07-0-UI1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2942	8096	12581	1.68	4.0E-60	AA299037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
1870	6990	12214	3.4	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1870	6990	12215	3.4	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1880	7000		22.16	3.0E-60	6031190	NT	Homo sapiens profilin (PHB) mRNA
4436	9555	14697	1.9	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
29	5240	10356	1.44	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1433	6560	11743	6.02	2.0E-60	Z11694.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
1735	6862	12064	1.24	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
1743	6870	12074	1.14	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
2671	7767	13019	1.01	2.0E-60	AW078005.1	EST_HUMAN	EST390114 MAGE resequences, MAGE Homo sapiens cDNA
3566	8707	13668	0.68	2.0E-60	4757867	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3889	9025	14183	0.86	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
520	5686	10818	2.73	1.0E-60	BE178586.1	EST_HUMAN	PM3-HIT0605-270200-001-e06 HIT0605 Homo sapiens cDNA
3879	9016	14172	0.92	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
4936	10045	15185	1.21	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1100	6238	11401	1.27	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
2631	7729	12985	1.01	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2806555 3'
2631	7729	12986	1.01	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2806555 3'
2917	8071		2.67	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
123	5322	10466	0.66	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
123	5322	10467	0.66	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
293	5453	10591	2.73	6.0E-61	BE406310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
812	5965	11127	1.88	6.0E-61	BE406310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1326	6455	11633	11.99	6.0E-61	AF119650.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1640	6788	11982	1.17	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3350145 5'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1660	6788	11983	3.34	6.0E-61	AA590033.1	EST_HUMAN	nm66h09.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
3288	8437	13598	8.59	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
357	5538	10679	0.65	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1692	8821	12020	3.02	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3008	8162	13319	2.26	5.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3181	8332	13495	1.46	5.0E-61	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3954	9089		1.55	5.0E-61	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4988	5538	10679	0.65	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4186	8312	14447	1.29	3.0E-61	BE396279.1	EST_HUMAN	601309785F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631220 6'
498	5865	10800	1.57	2.0E-61	8922828	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
1215	6347	11517	3.89	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1216	6347	11618	3.89	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1679	6808	12006	1.52	2.0E-61	NS3039.1	EST_HUMAN	yv53d11.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:246453 3' similar to gb.L25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);
2804	7703		1.41	2.0E-61	N39397.1	EST_HUMAN	Y03711.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270189 5'
434	5803		0.88	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
773	5927	11086	1.22	1.0E-61	5453828	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog) like (ORC2L), mRNA
1405	8533	11711	1.13	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1869	6989	12213	3.34	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2180	7293	12540	2.26	1.0E-61	AW827281.1	EST_HUMAN	xm11h09.y1 NCL_CGAP_L15 Homo sapiens cDNA clone IMAGE:2693369 5' similar to contains element
2766	7953	13119	1.57	1.0E-61	BE396393.1	EST_HUMAN	MSR1 repetitive element;
3357	8902	13670	0.88	1.0E-61	7662319	NT	601273613F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
3713	8851	14005	1.52	1.0E-61	BE174455.1	EST_HUMAN	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
4417	9537	14677	0.88	1.0E-61	4759249	NT	QV2-HT0577-140300-077-q06 HT0577 Homo sapiens cDNA
4417	9537	14678	0.88	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4826	9938	15079	9.22	1.0E-61	AW298181.1	EST_HUMAN	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4826	9938	15080	9.22	1.0E-61	AW298181.1	EST_HUMAN	UI-H-BWO-gt-b-08-0-UI.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4524	8942	14790	1.04	8.0E-62	AA830420.1	EST_HUMAN	UI-H-BWO-gt-b-08-0-UI.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
1108	6246	11409	1.12	7.0E-62	AV714334.1	EST_HUMAN	cc66h11.s1 NCL_CGAP_QCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW_P01_MLVRK
3490	8831	13788	0.7	7.0E-62	P17480	SWISSPROT	P31796 POL POLYPROTEIN;
							AV714334 DGB Homo sapiens cDNA clone DCBAMA08 5'
							NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)
							(AUTOANTIGEN NOR-90)

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2968	8122		1.44	6.0E-62	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
3365	8510		4.59	8.0E-62	11418255	NT	Homo sapiens CGI-56 protein (CGI-56), mRNA
415	5583	10731	5.02	5.0E-62	A1950528.1	EST_HUMAN	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2647204 3' similar to SW:GG96_HUMAN
2383	7489	12742	2.82	5.0E-62	AJ271735.1	NT	Q08379 GOLGIN-95; contains element MER22 repetitive element;
2383	7489	12743	2.82	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2552	7655	12905	1.11	5.0E-62	U39487.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2552	7655	12908	1.11	5.0E-62	U39487.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
3400	8544	13703	2.69	5.0E-62	4506758	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
4304	9426	14561	1.75	5.0E-62	AA431083.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4532	9650		0.96	5.0E-62	AW905887.1	EST_HUMAN	zw78e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
841	5993	11161	2.12	4.0E-62	AW161479.1	EST_HUMAN	P47245 NARDILYSIN ;
841	5993	11162	2.12	4.0E-62	AW161479.1	EST_HUMAN	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
842	5993	11161	2.44	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
842	5993	11162	2.44	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2435	7539	12792	4.32	4.0E-62	A1827900.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
2435	7539	12793	4.32	4.0E-62	A1827900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3380	8525		8.06	4.0E-62	A1827900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
73	5282	10420	0.7	3.0E-62	4557794	NT	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
3018	8172	13328	1.13	3.0E-62	AB040909.1	NT	wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
3018	8172	13329	1.13	3.0E-62	AB040909.1	NT	gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
3675	8814	13970	14.65	3.0E-62	X52853.1	NT	wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
4948	10057	15195	228.4	3.0E-62	AF229180.1	NT	gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
1234	6385	11538	2.82	2.0E-62	AL163284.2	NT	Homo sapiens keratin 18 (KRT18) mRNA
1046	6187	11354	1.22	1.0E-62	AF248540.1	NT	Homo sapiens neurofilament 2 (bilateral acoustic neuroma) (NF2) mRNA
1559	6688	11875	10.74	1.0E-62	L78810.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
							Homo sapiens alpha-amino acid decarboxylase semialdehyde synthase mRNA, complete cds
							Homo sapiens chromosome 21 segment HS21C084
							Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
							Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1811	6934	12149	1.99	1.0E-62	AA625207.1	EST_HUMAN	at70e11.1 Soares_Nhi-IMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1
2880	8034	13201	0.98	1.0E-62	AL039044.1	EST_HUMAN	CE034633
3405	8548		0.97	1.0E-62	AB040911.1	NT	DKFZp566F104_r1 568 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566F104 5'
4501	9620	14762	1.67	1.0E-62	8923201	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
336	5519	10555	2.1	9.0E-63	AW816405.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
4015	9148	14289	7.57	9.0E-63	AB002348.2	NT	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
4015	9148	14290	7.57	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
2354	7481	12717	18.96	8.0E-63	5031810	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
3443	8585	13746	3.27	8.0E-63	AF168349.1	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3443	8585	13747	3.27	8.0E-63	AF168349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4239	9364	14497	4.21	8.0E-63	AL163268.2	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
930	6078		3.87	7.0E-63	AI872137.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C068
3302	8449	13612	0.75	4.0E-63	AL163278.2	NT	wm55g11 x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'
3796	8923	14072	1.16	4.0E-63	AB014607.1	NT	Homo sapiens chromosome 21 segment HS21C078
3796	8923	14073	1.16	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
3796	8923	14073	1.16	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
1939	7068	12280	2.85	3.0E-63	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2740	7834	13087	2.12	3.0E-63	J00310.1	NT	Human Met-tRNA-I gene 1
2781	6373	11549	10.06	3.0E-63	5005963	NT	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
188	5383	10525	1.65	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
195	5390	10533	1.26	2.0E-63	4885226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
497	5694		1.72	2.0E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
827	5980	11146	2.95	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
1581	6710	11901	1.46	2.0E-63	AB030398.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1581	6710	11902	1.46	2.0E-63	AB030398.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1777	6903	12111	2.86	2.0E-63	BE140739.1	EST_HUMAN	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636103 5'
3135	8286	13443	1.74	2.0E-63	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3259	8418	13580	2.28	2.0E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3882	9018	14175	3	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4835	9947	15091	1.36	2.0E-63	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1527	5654	11840	1.29	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-znd11





Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3118	8270	13428	1.06	2.0E-64	4504088	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
3766	8903	14055	0.65	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGE resequences, MAGE Homo sapiens cDNA
3766	8903	14056	0.65	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGE resequences, MAGE Homo sapiens cDNA
255	5446	10584	1.7	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1789	5915	12122	66.19	1.0E-64	AI929419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb:121696_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element;
3498	8637	13804	4.48	1.0E-64	AF196779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha$ -
3572	8713	13873	1.18	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3572	8713	13874	1.18	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3877	9013	14170	0.86	1.0E-64	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1058	6199	11384	6.24	6.0E-65	AV721898.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC06 5'
1927	7046		40.69	6.0E-65	AA650929.1	EST_HUMAN	rib6d10.s1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:998379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
630	5790	10923	1.77	5.0E-65	AF084604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1360	6489	11669	1.51	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1360	6489	11670	1.51	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2138	7252	12498	0.99	5.0E-65	AB033768.1	NT	Homo sapiens hPAD-cdny10 mRNA for peptidylarginine deiminase type I, complete cds
3238	8388	13550	1.89	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3238	8388	13551	1.89	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
190	5385	10528	2.69	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
744	5900	11053	1.12	4.0E-65	AI268468.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8tc9weeks_2NbHP8b89W Homo sapiens cDNA clone IMAGE:1891800 3'
744	5900	11054	1.12	4.0E-65	AI268468.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8tc9weeks_2NbHP8b89W Homo sapiens cDNA clone IMAGE:1891800 3'
1080	6219	11385	1.97	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1498	6623	11811	21.94	4.0E-65	4506836	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2318	7426	12677	2.41	4.0E-65	BE221499.1	EST_HUMAN	hu25e04.x1 NCL_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
2318	7426	12678	2.41	4.0E-65	BE221499.1	EST_HUMAN	hu25e04.x1 NCL_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
3922	9058	14217	0.98	4.0E-65	AW993185.1	EST_HUMAN	RC2-BN0033-160200-013-a03 BN0033 Homo sapiens cDNA
5167	10265	15405	0.92	4.0E-65	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDIIT), mRNA
5167	10265	15406	0.92	4.0E-65	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDIIT), mRNA

Page 124 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
93	5303	10443	1.88	3.0E-65	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
94	5303	10443	1.37	3.0E-65	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1236	7870		27.41	3.0E-65	X78932.1	NT	H.sapiens HZF9 mRNA for zinc finger protein
1573	8701	11889	3.1	3.0E-65	4504628	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1834	6957	12179	1.46	3.0E-65	A1000882.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
2859	8113	13275	1.49	3.0E-65	D87078.2	NT	MSR1 repetitive element;
3260	8409	13572	0.8	3.0E-65	4504950	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
3701	8839	13993	1.47	3.0E-65	A1000892.1	EST_HUMAN	Homo sapiens laminin, beta 1 (LAMB1), mRNA
4518	9738	14874	1.39	3.0E-65	6912385	NT	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
3385	8529	13681	5.17	2.0E-65	BF680294.1	EST_HUMAN	MSR1 repetitive element;
86	5295	10836	2.98	1.0E-65	BF125544.1	EST_HUMAN	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPOCENA), mRNA
537	5703	10836	2.98	1.0E-65	7687495	NT	602155062F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295986 5'
2034	7152	12392	1.85	1.0E-65	AB040946.1	NT	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028501 5'
3354	8499	13667	1.15	1.0E-65	BE466881.1	EST_HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3973	9107	14255	2.73	1.0E-65	4504082	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3973	9107	14255	2.73	1.0E-65	4504082	NT	h224a09.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3208888 3'
4179	9305	14440	2.1	1.0E-65	AW029340.1	EST_HUMAN	Homo sapiens glycocalyx 4 (GPC4) mRNA
4179	9305	14441	2.1	1.0E-65	AW029340.1	EST_HUMAN	Homo sapiens glycocalyx 4 (GPC4) mRNA
70	5280	10416	1.38	9.0E-66	AL160311.1	NT	wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543162 3'
70	5280	10417	1.38	9.0E-66	AL160311.1	NT	wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
1361	6480	11671	2.88	9.0E-66	5031980	NT	Novel human gene mapping to chromosome 22
1361	6490	11672	2.88	9.0E-66	5031980	NT	Novel human gene mapping to chromosome 22
1494	6621		5.38	9.0E-66	M87299.1	NT	Homo sapiens 26S proteasome-associated pad1 homologue (POH1) mRNA
4344	9466	14802	1.18	8.0E-66	A1924653.1	EST_HUMAN	Homo sapiens 26S proteasome-associated pad1 homologue (POH1) mRNA
4344	9466	14803	1.18	6.0E-66	A1924653.1	EST_HUMAN	Human transposon-like element, partial
4344	9466	14804	1.18	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
1376	6504	11686	1.84	5.0E-66	BE064410.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
5091	10191	15330	2.25	5.0E-66	BE838644.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
							CE18595;
							CE18595;
							wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
							CE18595;
							wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
							CE18595;
							RC4-BT0311-141189-011-r06 BT0311 Homo sapiens cDNA
							601881592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'

Page 125 of 214

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon. SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5091	10191	15331	2.25	5.0E-66	BE898644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
791	5945	11105	0.87	4.0E-66	6679816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1). mRNA
2257	7367	12823	1.81	4.0E-66	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2449	7553		2.75	4.0E-66	AJ223384.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4751	9894		4.83	4.0E-66	9635487	NT	Human endogenous retrovirus, complete genome
1436	6563	11747	26.39	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1436	6563	11748	26.39	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1984	7101	12332	1.1	3.0E-66	N55323.1	EST_HUMAN	Y27g12.1 Soares multiple sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B-1/H2B.2. [2] PIR:B56612;
1984	7101	12333	1.1	3.0E-66	N55323.1	EST_HUMAN	Y27g12.1 Soares multiple sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B-1/H2B.2. [2] PIR:B56612;
1984	7101	12334	1.1	3.0E-66	N55323.1	EST_HUMAN	Y27g12.1 Soares multiple sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B-1/H2B.2. [2] PIR:B56612;
2689	7765	13016	4.38	3.0E-66	11141880	NT	Homo sapiens TGF(beta)-induced transcription factor 2 (TGIF2), mRNA
3093	8248	13396	6.5	3.0E-66	7662223	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
50	5282	10387	2	2.0E-66	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
50	5282	10388	2	2.0E-66	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
421	5208	10320	0.99	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
421	5208	10321	0.99	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1839	6960	12183	2.4	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3506	8947	13813	1.15	2.0E-66	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3745	8883	14033	1.02	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4625	9743	14896	5.12	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
4625	9743	14897	6.12	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
1697	6825		1.77	1.0E-66	BE887173.1	EST_HUMAN	601508376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909931 5'
2850	8015	13180	1.52	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADCC07 5'
2850	8015	13181	1.52	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADCC07 5'
4364	8015	13190	2.97	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADCC07 5'
4364	8015	13181	2.97	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADCC07 5'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4891	10002		0.61	8.0E-67	M78158.1	EST_HUMAN	EST01750 Subtracted Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCPN31 similar to L1 repetitive element
378	5587	10732	1.89	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1392	6520	11700	2.26	7.0E-67	AA383418.1	EST_HUMAN	EST96812 Testis 1 Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK353
1569	6697	11884	4.25	7.0E-67	W85947.1	EST_HUMAN	zh56p05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1569	6697	11885	4.25	7.0E-67	W85947.1	EST_HUMAN	zh56p05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2027	7144	12383	2.29	7.0E-67	7657243	NT	Homo sapiens Inositol 1,3,4-trisphosphate 5/8 kinase (ITPK1), mRNA
2027	7144	12384	2.29	7.0E-67	7657243	NT	Homo sapiens Inositol 1,3,4-trisphosphate 5/8 kinase (ITPK1), mRNA
2771	5587	10732	2.33	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
558	5723	10854	8.35	6.0E-67	X68998.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
796	5980	11110	1.66	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1277	6408	11580	0.99	6.0E-67	Y14320.1	NT	Homo sapiens PMP69 gene, exons 3,4,5,6 & 7
3147	8298	13456	1.28	6.0E-67	4508434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3419	8561	13718	1.21	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3419	8561	13719	1.21	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4097	9226	14361	0.88	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4097	9226	14362	0.88	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4673	9789	14934	2.84	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4673	9789	14935	2.84	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5157	10257	15395	0.99	6.0E-67	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
5157	10257	15396	0.99	6.0E-67	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
3206	8357	13518	2.93	5.0E-67	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
1333	6462	11642	3.95	4.0E-67	R90819.1	EST_HUMAN	yn02d11.r1 Soares adult brain N2b44B55Y Homo sapiens cDNA clone IMAGE:167253 5'
2774	5792	10926	1.33	3.0E-67	AA333768.1	EST_HUMAN	EST37803 Embryo, 9 week Homo sapiens cDNA 5' end
3435	8577	13737	1.12	3.0E-67	BE064410.1	EST_HUMAN	RC4-BT0311-1471198-011-H06 BT0311 Homo sapiens cDNA
4653	9779	14923	2.26	3.0E-67	AW869159.1	EST_HUMAN	MF3-SN0066-040500-008-f01 SN0066 Homo sapiens cDNA
4690	9806		0.92	3.0E-67	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
184	5379	10520	1.33	2.0E-67	BE346354.1	EST_HUMAN	hw16g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9 CE09617;
846	5997	11168	3.92	2.0E-67	AW816405.1	EST_HUMAN	QV4-ST0234-181198-037-05 ST0234 Homo sapiens cDNA
1106	5244		1.98	2.0E-67	AF167460.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4

Page 127 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1892	7011	12232	1.51	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805976 5' similar to TR:084892 084892 KIAA0798 PROTEIN ;
1892	7011	12233	1.51	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805976 5' similar to TR:084892 084892 KIAA0798 PROTEIN ;
2221	7333	12586	1.11	2.0E-67	11422946	NT	Homo sapiens hypothetical protein DJ462023.2 (DJ462023.2), mRNA
2221	7333	12587	1.11	2.0E-67	11422946	NT	Homo sapiens hypothetical protein DJ462023.2 (DJ462023.2), mRNA
2364	7470	12726	2.48	2.0E-67	AF305631.1	NT	Homo sapiens KRAB zinc finger protein ZFOR mRNA, complete cds
2409	7515	12765	2.21	2.0E-67	4758795	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
3449	8501	13765	3.92	2.0E-67	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
3977	9111	14259	2.44	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
250	5441	10581	4.73	1.0E-67	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
708	5863	11010	1.9	1.0E-67	AA702794.1	EST_HUMAN	z90b04.s1 Soares_fetal_liver_spleen_1NF1S_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4679	9795	14040	0.8	1.0E-67	BF439247.1	EST_HUMAN	na6b1f08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
2156	7269	12517	4.77	8.0E-68	BE970732.1	EST_HUMAN	601448556F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3848	8984	14139	5.22	8.0E-68	AA209455.1	EST_HUMAN	zq82h10.r1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN ;
3848	8984	14140	5.22	8.0E-68	AA209455.1	EST_HUMAN	zq82h10.r1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN ;
1899	7018		1.22	6.0E-68	AW503842.1	EST_HUMAN	UI-HF-BN0-alb-c-07-Q-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
803	7866	11118	0.72	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
803	7866	11119	0.72	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
820	5973	11135	3.62	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
820	5973	11136	3.62	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2741	7835	13088	36.25	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3125	8277	13433	2.97	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4152	9278		0.76	5.0E-68	4828987	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
2498	7602	12849	1.27	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2498	7602	12850	1.27	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
3084	8217		1.12	4.0E-68	AW207003.1	EST_HUMAN	UI-H-B11-af-c-08-Q-UI.s1 NC1 CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721399 3'
4950	10068		19.6	4.0E-68	P04405	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
3638	8777	13832	5.79	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
2825	10313		32.61	2.0E-68	D00522.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3998	9132	14276	0.7	2.0E-68	BE675766.1	EST_HUMAN	7f15f02.x1 NCI_CGAP CLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:O80828 O80828
4653	9770	14916	2.05	2.0E-68	AB008881.1	NT	HYPOTHETICAL 88.8 KD PROTEIN. ; Homo sapiens gene for activin receptor type IIB, complete cds
294	5482	10624	11.03	1.0E-68	AW816405.1	EST_HUMAN	QV4-ST0234-181189-037-05 ST0234 Homo sapiens cDNA
2232	7344	12598	1.34	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2232	7344	12699	1.34	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2720	7815	13071	1.15	1.0E-68	AW451832.1	EST_HUMAN	UHH-BI3-alk-f-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737272 3'
3985	9119	14266	1.54	1.0E-68	BE296032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3332344 5'
5055	10157	15288	1.38	1.0E-68	BE296032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3332344 5'
20	5231	10343	8.71	9.0E-69	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
20	5231	10344	8.71	9.0E-69	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1029	6170	11335	1.66	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1029	6170	11336	1.66	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4100	9229	14368	0.68	9.0E-69	4757887	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3367	8512		1.14	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
518	5684		0.98	4.0E-69	AI873630.1	EST_HUMAN	wm26h11.x1 NCI_CGAP_Uk4 Homo sapiens cDNA clone IMAGE:2437125 3'
384	5593	10739	5.27	3.0E-69	BE258012.1	EST_HUMAN	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
609	5769	10898	1.96	3.0E-69	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
1570	6698		1.54	3.0E-69	T80514.1	EST_HUMAN	yd08a02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24880 5' similar to SP:A48938
4940	10050	15188	0.97	3.0E-69	AB037732.1	NT	A48836 SPEGF III-EGF REPEAT-CONTAINING FIBROPELIN-LIKE PROTEIN - SEA URCHIN ; Homo sapiens mRNA for KIAA1311 protein, partial cds
5126	9189	14330	0.95	3.0E-69	AI765888.1	EST_HUMAN	wh66g08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385758 3'
124	5571	10718	2.22	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
124	5571	10719	2.22	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
404	5571	10718	4.66	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
404	5571	10719	4.66	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1893	7012	12234	2.34	2.0E-69	BE257857.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
2806	7982		3.36	2.0E-69	AA431157.1	EST_HUMAN	zw71g02.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:781692 5'
1718	6845	12048	1.61	1.0E-69	AF053763.1	NT	Rattus norvegicus brain specific contactin-binding protein CSP90 mRNA, partial cds
2313	7937	12872	2.34	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
4352	9474	14612	1.7	8.0E-70	L77566.1	NT	Homo sapiens DGSH mRNA, 3' end
1826	6948	12169	3.57	7.0E-70	AI497807.1	EST_HUMAN	fm89f01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163305 3'
1826	6948	12170	3.57	7.0E-70	AI497807.1	EST_HUMAN	fm89f01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163305 3'

Page 129 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1935	7054	12276	1.88	7.0E-70	AA282955.1	EST_HUMAN	zf15h04.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
2058	7172		8.1	7.0E-70	5031668	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4202	9327	14459	3.42	7.0E-70	4787723	NT	Homo sapiens adenylylate cyclase 3 (ADCY3) mRNA
872	6023	11194	3.49	6.0E-70	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2125	7239	12482	5.6	6.0E-70	M30638.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2478	7584	12834	2.07	6.0E-70	8923899	NT	Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC55907), mRNA
2523	7942	12871	3.38	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2523	7942	12872	3.38	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
1802	6730	11921	5.33	3.0E-70	BE071796.1	EST_HUMAN	RCO-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
1802	6730	11922	5.33	3.0E-70	BE071796.1	EST_HUMAN	RCO-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
5137	10237	16373	0.94	3.0E-70	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
37	5248	10368	1.24	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
687	5845	10985	13.85	2.0E-70	N42161.1	EST_HUMAN	y07a10.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
687	5845	10986	13.85	2.0E-70	N42161.1	EST_HUMAN	y07a10.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
703	5860	11009	2.51	2.0E-70	A1246899.1	EST_HUMAN	qx51h01.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1022	6163	11329	1.75	2.0E-70	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1188	6320	11488	4.33	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1188	6320	11489	4.33	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1754	6880	12086	1.41	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2298	7407		4.84	2.0E-70	AA054010.1	EST_HUMAN	zf48g04.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
2460	7584	12817	1.35	2.0E-70	AB011173.1	NT	P03345 GAG POLYPROTEIN ;
3797	8934	14081	2	2.0E-70	AL133207.2	NT	Homo sapiens mRNA for KIAA0601 protein, partial cds
4023	9155	14299	4.56	2.0E-70	M69181.1	NT	Novel human gene mapping to chromosome X
4164	9280	14426	0.9	2.0E-70	L78810.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
4164	9280	14427	0.9	2.0E-70	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
3374	8519		3.07	1.0E-70	4507476	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
2192	7304	12554	31.81	5.0E-71	AF055322.1	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
4092	8221	14358	1.07	5.0E-71	AW819405.1	EST_HUMAN	Homo sapiens SP100-HMG nuclear autoantigen (SP100), mRNA, complete cds
100	5309	10449	0.9	4.0E-71	4507592	NT	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
							Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA

Page 130 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
347	5530	10668	331.53	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
347	5530	10669	331.53	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2845	8000	13159	1.01	4.0E-71	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2845	8000	13160	1.01	4.0E-71	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2853	8008	13168	2.01	4.0E-71	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4406	9526	14666	5.18	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4971	10079	15216	5.78	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOUL), mRNA
1233	6364	11537	6.91	2.0E-71	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
637	5798	10932	1.78	1.0E-71	A1077927.1	EST_HUMAN	oy15e03.s1 Scores, senescent, fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:1685816 3' similar to contains LOR1 b2 LOR1 repetitive element;
941	6089	11257	3.28	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1101	6239	11402	3.42	1.0E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1346	6474	11654	8.13	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pik230) mRNA, complete cds
2075	7191	12434	3.22	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2075	7191	12435	3.22	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2854	7762	13001	2.34	1.0E-71	7657153	NT	Homo sapiens hairyenhancer-of-split related with YRPW motif-like (HEYL), mRNA
3484	8625	13792	2	1.0E-71	AF119655.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3582	8723	13880	6.81	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3582	8723	13881	5.81	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3626	8765	13920	0.83	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3626	8765	13921	0.83	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3722	8880	14013	2.47	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATTRN) gene, exon 19
4449	9568	14709	1.82	1.0E-71	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
407	5574	10721	0.89	9.0E-72	A1857635.1	EST_HUMAN	wk95g03.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705
407	5574	10722	0.89	9.0E-72	A1857635.1	EST_HUMAN	HYPOHETICAL 38.6 KD PROTEIN ; contains Alu repetitive element;
4098	9216	14350	1.01	7.0E-72	4501866	NT	wk95g03.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705
4098	9216	14350	1.01	7.0E-72	4501866	NT	HYPOHETICAL 38.6 KD PROTEIN ; contains Alu repetitive element;
4088	9216	14351	1.61	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4088	9216	14351	1.61	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA



Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4088	9216	14352	1.61	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
62	5273	10407	2.15	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
62	5273	10408	2.15	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
63	5273	10407	8.82	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
63	5273	10408	8.82	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
1140	6277		1.83	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
4790	9903		1.2	4.0E-72	11034844	NT	Homo sapiens hypothetical protein DJ1057B20.2 (DJ1057B20.2), mRNA
19	5230	10342	2.05	3.0E-72	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
904	6064		0.93	3.0E-72	AA723823.1	EST_HUMAN	ah63a06.e1 Soares_testis_NHT Homo sapiens cDNA clone 1310280 3'
1156	6292	11455	7.41	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1156	6292	11456	7.41	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1196	6330	11497	1.48	3.0E-72	U80226.1	NT	Human gamma-aminobutylic acid transaminase mRNA, partial cds
1196	6330	11498	1.48	3.0E-72	U80226.1	NT	Human gamma-aminobutylic acid transaminase mRNA, partial cds
1534	6661	11847	1.1	3.0E-72	BE242161.1	EST_HUMAN	TCAAP1E1252 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HQSC project=TCAA Homo sapiens cDNA clone TCAAP1252
3046	8200	13356	10.6	3.0E-72	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3262	8411	13573	2.73	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20586 (FLJ20586), mRNA
3801	8536	14083	2.78	3.0E-72	S77589.1	NT	TCR V delta 2-C alpha =T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4395	9515	14656	1.1	3.0E-72	AF143892.1	NT	Human, precursor B-cell line REH, mRNA Partial, 211 nt
4395	9515	14657	1.1	3.0E-72	AF143892.1	NT	Homo sapiens thiodoxin-like protein (TXNL) gene, exon 3
4518	9636	14781	2.83	3.0E-72	11416196	NT	Homo sapiens thiodoxin-like protein (TXNL) gene, exon 3
4732	9845	14990	1.34	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
4732	9845	14991	1.34	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
4899	10010	15155	1.06	3.0E-72	AIG54337.1	EST_HUMAN	wb31a08.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2307254 3'
2067	7183	12423	1.08	1.0E-72	AA846225.1	EST_HUMAN	ah33402.s1 Soares_parathyroid_tumor_NbthPA Homo sapiens cDNA clone IMAGE:1387395 3'
1472	6599	11785	1.63	9.0E-73	AW374988.1	EST_HUMAN	MRO-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA
1040	6180	11345	1.57	8.0E-73	AW071755.1	EST_HUMAN	ws55606.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR:Q59050
1428	6555	11737	2.38	8.0E-73	AJ024877.1	EST_HUMAN	Q59050 HYPOTHETICAL PROTEIN MJ1656 ;
1135	6272	11436	1.92	7.0E-73	8923290	NT	ov499108.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639743 3'
							Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA

Page 132 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3283	8432	13594	0.89	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
4921	10031		1.81	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
153	5350		2.16	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
1346	6475	11855	2.17	3.0E-73	AW843789.1	EST_HUMAN	CMO-CN0044-260100-164408 CN0044 Homo sapiens cDNA
1873	6993	12218	1.47	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1873	6993	12219	1.47	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
852	6003	11174	2.53	2.0E-73	AF139897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds
1950	7088		3.26	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
2271	7381		1.06	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3161	8312	13473	3.99	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3537	8679	13840	0.63	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3537	8679	13841	0.63	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
4411	9531		1.08	2.0E-73	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
1793	5919	12129	2.37	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
2458	7582	12814	1.05	1.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
739	5895	11047	2.05	8.0E-74	4557426	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
1953	7070	12294	2.19	7.0E-74	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
3309	8456	13618	1.22	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1123	6281	11426	3.46	6.0E-74	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
2294	7403	12654	89.23	6.0E-74	BE388260.1	EST_HUMAN	601283521 F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2294	7403	12655	89.23	6.0E-74	BE388260.1	EST_HUMAN	601283521 F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2827	7982	13144	1.2	6.0E-74	AW014039.1	EST_HUMAN	UI-H-B10-aah-h-03-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
2827	7982	13145	1.2	6.0E-74	AW014039.1	EST_HUMAN	UI-H-B10-aah-h-03-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3692	8830	13984	1.39	6.0E-74	BE048946.1	EST_HUMAN	h54e11.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3132332 3'
3692	8830	13985	1.39	6.0E-74	BE048946.1	EST_HUMAN	h54e11.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3132332 3'
5011	10114	15244	1	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S. cerevisiae CHL1-like helicase) (DDX11) mRNA
5011	10114	15245	1	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S. cerevisiae CHL1-like helicase) (DDX11) mRNA
908	6056	11225	2.51	5.0E-74	AW020986.1	EST_HUMAN	df17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2663	7759		5.84	5.0E-74	AW352756.1	EST_HUMAN	PM0-CT0289-271099-001-107 CT0289 Homo sapiens cDNA

Page 133 of 214  
Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
277	5486	10609	5.66	4.0E-74	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
853	6004	11175	11.32	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1966	7083	12307	1.19	4.0E-74	AB028998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1966	7083	12308	1.19	4.0E-74	AB028998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2064	7180	12419	11.24	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2064	7180	12420	11.24	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2123	7238	12481	1.98	4.0E-74	AB032894.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2404	7510	12760	7.16	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3083	8216	13370	6.64	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3514	8655	13821	0.83	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4038	9169	14310	1	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4596	9704	14842	0.87	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5057	10159	15260	1.18	4.0E-74	4504326	NT	Homo sapiens hydroxycy-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
5057	10159	15261	1.18	4.0E-74	4504326	NT	Homo sapiens hydroxycy-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
959	6107	11276	397.42	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
959	6107	11277	397.42	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1177	6312	11480	1.04	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-T47D
1248	6378	11557	3.01	2.0E-74	AB050528.1	EST_HUMAN	wx51e07 x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
1608	6736	11929	3.81	2.0E-74	4885198	NT	Q08379 GOLGIN-95 ; contains element MER22 repetitive element ;
1608	6736	11930	3.81	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2566	7667	12922	7.73	2.0E-74	AB057280.1	EST_HUMAN	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
4993	10069	15229	2.72	2.0E-74	AL355092.1	NT	PT2.1_15_G11.r.tumor2 Homo sapiens cDNA 3'
4993	10069	15230	2.72	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
52	5264	10391	2.55	1.0E-74	7657334	NT	Novel human gene mapping to chromosome 22
335	5518	10654	3.25	1.0E-74	AW816405.1	EST_HUMAN	Homo sapiens Mississippin/NIK-related kinase (MINK), mRNA
499	5666	10801	1.38	1.0E-74	8922829	NT	QV4-STU234-181199-037-405 ST0234 Homo sapiens cDNA
							Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
506	5672	10806	13.77	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
599	5761	10889	1.72	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
1000	6146	11313	2.39	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2208	7320	12571	3.57	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3117	8269	13425	3.47	1.0E-74	4758697	NT	Homo sapiens mannose 6-phosphate isomerase, alpha, class 2A, member 1 (MAN2A1), mRNA
3895	9031	14190	0.87	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3895	9031	14191	0.87	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3941	9077	14231	5.54	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4039	9170	14311	0.9	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0642-270300-019-408 BT0642 Homo sapiens cDNA
4241	9366	14499	0.72	1.0E-74	BE467769.1	EST_HUMAN	h273h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:50511.12
2607	7706		2.28	8.0E-75	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
2299	7408	12659	1.55	6.0E-75	A1817415.1	EST_HUMAN	wk38a08.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4
108	5312	10451	1.9	4.0E-75	BE081333.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (HUMAN);
458	5626		1.35	4.0E-75	N36757.1	EST_HUMAN	QV1-BT0632-210200-079-e02 BT0632 Homo sapiens cDNA
1776	6902	12110	1.14	4.0E-75	AW897230.1	EST_HUMAN	yx90h08.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:268055 5'
2811	7867	13127	5.46	4.0E-75	BE409464.1	EST_HUMAN	CMO-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA
3483	8624	13791	1.18	4.0E-75	8922637	NT	601303863F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
1003	6149	11316	3.28	3.0E-75	AF157623.1	NT	Homo sapiens hypothetical protein FLJ10747 (FLJ10747), mRNA
1004	6149	11316	2.31	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1850	6971	12192	1.97	3.0E-75	AB011153.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
2400	7506	12755	2.07	3.0E-75	4759153	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2993	8148	13308	0.81	3.0E-75	AL163201.2	NT	Homo sapiens synaptonemal-associated protein, 29kD (SNAP29) mRNA
3172	8323	13484	1.18	3.0E-75	AB011153.1	NT	Homo sapiens chromosome 21 segment HS21C001
3332	8478	13642	0.65	3.0E-75	M72393.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3332	8478	13643	0.65	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4139	9267	14407	1.34	3.0E-75	D81675.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4414	9534	14673	1.22	3.0E-75	7662421	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
2278	7398	12639	15.13	1.0E-75	AW108135.1	EST_HUMAN	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
2912	8066	13239	3.84	1.0E-75	X62221.1	NT	xg60a02.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.11
43	5255	10375	7.63	9.0E-76	A1852848.1	EST_HUMAN	PTR7 repetitive element; H.sapiens ERCC2 gene, exons 1 & 2 (partial) wb30b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;

Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
43	5255	10376	7.93	9.0E-76	AI652648.1	EST_HUMAN	wb30b10.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
938	6086	11263	0.77	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HFI1) mRNA
938	6088	11254	0.77	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HFI1) mRNA
776	5930	11089	2.91	7.0E-76	5016092	NT	Homo sapiens dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3276	8425	13886	2.55	7.0E-76	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3282	8431	13863	6.25	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
4360	9472	14609	4.75	7.0E-76	4507184	NT	Homo sapiens septaplatin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4350	9472	14610	4.75	7.0E-76	4507184	NT	Homo sapiens septaplatin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1237	6367		72.97	6.0E-76	BE396253.1	EST_HUMAN	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
1947	7065	12288	28.9	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1947	7065	12289	28.9	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1947	7065	12290	28.9	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
628	5788	10920	1.96	3.0E-76	BF516262.1	EST_HUMAN	UIH-BW1-amz-b-04-0-UJ.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
628	5788	10921	1.66	3.0E-76	BF516262.1	EST_HUMAN	UIH-BW1-amz-b-04-0-UJ.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1612	6740	11934	11.26	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1612	6740	11935	11.26	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3410	8553	13711	5.9	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3410	8553	13712	5.9	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
4055	9185	14327	1.33	3.0E-76	BE348693.1	EST_HUMAN	h87f12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151823 3' similar to TR:O94886 O94886 KIAA0792 PROTEIN ;
279	5468	10611	1.59	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
340	5523	10658	2.51	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
340	5523	10659	2.51	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
460	5628		1.09	2.0E-76	4557662	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
588	5750	10878	2.7	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1032	6173	11341	1.89	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1650	6678	11865	1.85	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1550	6678	11866	1.95	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
2804	7960	13123	1.86	2.0E-76	P23266	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3279	8428	13590	2.04	2.0E-76	AA445992.1	EST_HUMAN	zw64e02.s1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;

Page 136 of 214  
Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3279	8428	13591	2.04	2.0E-76	AA445992.1	EST_HUMAN	zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780386 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
3749	8888	14037	0.6	2.0E-76	AA400700.1	EST_HUMAN	zu70g11.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743396 5' similar to WP:R05D3.2 CE00281 ;
4106	5468	10611	1.33	2.0E-76	DB4295.1	NT	Human mRNA for possible protein TPRDII, complete cds
4929	10035	15176	5.95	2.0E-76	AW879618.1	EST_HUMAN	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
4273	9397	14536	4.94	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4273	9397	14537	4.94	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
183	5377	10518	4.2	8.0E-77	R83144.1	EST_HUMAN	yp11hu2.r1 Soares breast 3NbrHst Homo sapiens cDNA clone IMAGE:187155 5' similar to SP:ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1 ;
4496	9815	14756	1.32	8.0E-77	BF205181.1	EST_HUMAN	601866926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
1934	7053	12275	1.51	7.0E-77	AA825755.1	EST_HUMAN	zu81g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2388	7494	12747	8.1	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2388	7494	12748	8.1	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
260	6450	10589	3.18	6.0E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1143	6280	11444	1.27	8.0E-77	AW957753.1	EST_HUMAN	EST369823 MAGE cDNAs, MAGE Homo sapiens cDNA
1557	6686	11874	2.81	8.0E-77	AI204066.1	EST_HUMAN	qe77h12.x1 Soares_fetal_lung_NbrHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
1239	6369	11542	1.91	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GOK) gene, exon 2
1369	6497	11680	2.47	5.0E-77	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2646	7744	12997	2.86	5.0E-77	AF162666.1	NT	Homo sapiens tousel-like kinase 1 (TLK1) mRNA, complete cds
2725	7820	13075	2.78	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3508	8649	13616	1.22	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18), mRNA
4913	10023	15167	2.57	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G1728 5'
3678	8817	13974	1.05	4.0E-77	AL449758.1	EST_HUMAN	AL449758 Homo sapiens fetal brain (Stavrides GS) Homo sapiens cDNA
1974	7091	12320	1.68	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1974	7091	12321	1.58	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1359	6489	11688	2.58	2.0E-77	AV764617.1	EST_HUMAN	Homo sapiens MDS Homo sapiens cDNA clone MDSBTF10 5'
1442	6570	11757	9.94	2.0E-77	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
2094	7209	12455	2.55	2.0E-77	7706315	NT	Homo sapiens CGH-79 protein (LOC51634), mRNA
2556	7643	12610	3.86	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2556	7643	12611	3.86	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4006	9139	14280	2.06	2.0E-77	BE044316.1	EST_HUMAN	h043b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;

Page 137 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4390	9510	14852	0.8	2.0E-77	AI613519.1	EST_HUMAN	hw22g02.x1 NCI_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245 O65245 F21E10.7 PROTEIN ;
4390	9510	14653	0.8	2.0E-77	AI613516.1	EST_HUMAN	hw22g02.x1 NCI_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245 O65245 F21E10.7 PROTEIN ;
4559	9687		1.29	2.0E-77	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4734	9847	14993	3.28	2.0E-77	AA853025.1	EST_HUMAN	ns88g12.s1 NCI_CGAP_Py2 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29. [1]; contains element MSR1 repetitive element ;
42	5253	10371	0.91	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
42	5253	10372	0.91	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
270	5460	10600	3.44	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
270	5460	10601	3.44	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
876	7903	11199	5.89	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
876	7903	11200	5.89	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1922	7041	12262	2.1	1.0E-77	AW058119.1	EST_HUMAN	hw63e05.x1 Soares_thymus_NH-FTh Homo sapiens cDNA clone IMAGE:2536160 3'
2421	7528	12779	1.28	1.0E-77	AB023024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3017	8171	13327	2.24	1.0E-77	4503300	NT	Homo sapiens 2,4-dienyl CoA reductase 1, mitochondrial (DEOR1), mRNA
4330	9452	14586	3.21	1.0E-77	7708299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
4498	9617	14758	17.67	1.0E-77	AJ226041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4819	9737	14875	1.92	1.0E-77	9552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
4662	9778	14922	1.6	1.0E-77	AI273014.1	EST_HUMAN	q009g04.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1981110 3'
4851	9963	15108	1.07	1.0E-77	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
4944	9695	14734	0.87	1.0E-77	4768063	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
5051	10153	15284	1.49	1.0E-77	7661849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5051	10153	15285	1.49	1.0E-77	7661849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
82	5291	10431	1.88	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354.5'
92	5291	10432	1.88	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354.5'
215	5409	10549	1.15	5.0E-78	11422466	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2634	7634	12882	4.52	5.0E-78	AW679424.1	EST_HUMAN	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP.Y48B6A.6
3366	8511	13678	3.9	5.0E-78	M55586.1	NT	Human collagenase type IV (CLG4) gene, exon 6
1138	6275	11439	1.7	4.0E-78	AL043314.2	EST_HUMAN	DKFZb434N0323.J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZb434N0323 5'
1533	8660	11846	1.38	4.0E-78	AL355841.1	NT	Novel human gene mapping to chromosome 22
1661	8789	11984	1.52	4.0E-78	AI985094.1	EST_HUMAN	wr97b12.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2495615 3' similar to SW.WAP_PIG
2296	7405	12657	22.41	4.0E-78	AF107405.1	NT	O46655 WHEY ACIDIC PROTEIN PRECURSOR;
4299	9421	14553	1.52	4.0E-78	7656876	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4740	9853	14999	1.57	4.0E-78	4505803	NT	Homo sapiens syncytin (LOC30819), mRNA
4740	9853	15000	1.57	4.0E-78	4505803	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
166	5353	10492	2.72	3.0E-78	AF095801.1	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
156	5353	10493	2.72	3.0E-78	AF095801.1	NT	Homo sapiens eRF1 gene, complete cds
2279	7389	12639	1.84	3.0E-78	4502142	NT	Homo sapiens eRF1 gene, complete cds
2393	7499	12750	1.36	3.0E-78	7706705	NT	Homo sapiens apoptosis inhibitor 3 (API3) mRNA
3199	8350	13513	0.95	3.0E-78	4507164	NT	Homo sapiens SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA
3744	8882		1.65	3.0E-78	AU140604.1	EST_HUMAN	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
3793	8930	14078	0.74	3.0E-78	4507334	NT	AU140604 PLACE3 Homo sapiens cDNA clone PLACE3000373 5'
4080	8930	14078	0.62	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
3098	8261		2.33	2.0E-78	U04489.1	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
3989	9123		1.51	2.0E-78	AA311872.1	EST_HUMAN	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4667	9783	14927	3.72	9.0E-79	11626891	NT	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
4833	9945	15088	3.54	9.0E-79	BE000837.1	EST_HUMAN	Homo sapiens peptide YY (PYY), mRNA
3723	8861	14014	1.12	8.0E-79	AL163210.2	NT	RG2-BN0074-090300-014-e12 BN0074 Homo sapiens cDNA
4468	9587	14725	1.44	8.0E-79	D28476.1	NT	Homo sapiens chromosome 21 segment HS21C010
5128	10228	15363	0.67	8.0E-79	8867387	NT	Human mRNA for KIAA0045 gene, complete cds
3235	8385	13547	11.83	7.0E-79	BE619848.1	EST_HUMAN	Human mRNA for KIAA0045 gene, complete cds
3166	8307		1.45	4.0E-79	8922325	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
311	5497	10637	1.68	3.0E-79	AF114488.1	NT	601472766T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876657 3'
979	6125	11295	3.13	3.0E-79	AF232708.1	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
3072	8225	13376	1.84	3.0E-79	U08410.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds
285	5474		0.82	2.0E-79	H63129.1	EST_HUMAN	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cin) gene, complete cds
633	5794	10928	1.36	2.0E-79	BE379826.1	EST_HUMAN	Human zinc finger protein ZNF131 mRNA, partial cds
							yr48f03.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:208541 3'
							601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'



Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
929	6077	11246	2.08	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1037	6178		0.89	2.0E-79	AB23747.1	EST_HUMAN	h18h07.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2118685 3'
1799	6924	12134	0.97	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1799	6924	12135	0.97	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1886	7006	12226	2	2.0E-79	7662255	NT	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA
2132	7246	12490	5.6	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2132	7246	12491	5.6	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2176	7289	12636	2.64	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2291	7400	12663	6.4	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
2345	7648	12897	2.34	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
2345	7648	12898	2.34	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
2677	7774	13025	1.18	2.0E-79	AB023154.1	NT	Homo sapiens mRNA for KIAA0937 protein, partial cds
4136	9264	14403	1.27	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
5197	10294	15431	1.23	2.0E-79	11421865	NT	Homo sapiens sodium calcium exchanger (NCKX3), mRNA
3124	8276	13431	7.56	9.0E-80	AA725848.1	EST_HUMAN	al23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3124	8276	13432	7.66	9.0E-80	AA725848.1	EST_HUMAN	al23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3687	8727		1.21	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
4934	10044	15184	1.07	7.0E-80	H04819.1	EST_HUMAN	y49d02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152067 5'
901	6051	11221	2.38	6.0E-80	AI422197.1	EST_HUMAN	tf58d02.x1 NCL CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW-NUJEM_HUMAN
1655	6783	11976	2.63	6.0E-80	U64898.1	NT	Q16795 NADH-UBIQUINONE OXIDOREDUCTASE, 39 KD SUBUNIT PRECURSOR ;
2272	7382	12629	3.33	6.0E-80	6631094	NT	Homo sapiens NRD convertase mRNA, complete cds
2272	7382	12630	3.33	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4259	9384	14519	1.05	6.0E-80	AB032931.1	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4259	9384	14520	1.05	6.0E-80	AB032931.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
586	5748	10877	34.63	5.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
836	5988	11156	2.08	5.0E-80	AF108930.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
836	5988	11167	2.08	5.0E-80	AF108930.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1191	6325		0.97	5.0E-80	X91647.1	NT	H. sapiens nex1 gene (exon 12)
1468	6595		1.14	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2341	7448	12702	1.26	5.0E-80	U89358.1	NT	Human (3)mbt protein homolog mRNA, complete cds
2408	7514	12764	1.86	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2755	7849	13104	8.85	5.0E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3F-J) mRNA
4013	9146	14287	0.97	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4013	9146	14288	0.97	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4933	10043	15183	1.32	5.0E-80	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
214	5408		10.59	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4876	9792	14938	1.3	3.0E-80	BF085009.1	EST_HUMAN	PM0-GN0018-040900-002-ED3 GN0018 Homo sapiens cDNA
4883	8994		3.62	3.0E-80	BE817465.1	EST_HUMAN	QV4-BN0263-040600-241-g10 BN0263 Homo sapiens cDNA
1810	6933	12148	3.63	2.0E-80	R35321.1	EST_HUMAN	yg65a08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:38060 5'
1871	6991	12216	3.99	2.0E-80	AL444821.1	EST_HUMAN	RET4B7 subtracted retina cDNA library Homo sapiens cDNA clone RET4B7
2047	7163	12402	15.22	2.0E-80	AL043116.2	EST_HUMAN	DKFZp434D1323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1323 5'
338	5521		1.4	1.0E-80	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
800	5954	11114	1.98	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1958	7075		1.44	1.0E-80	AF732656.1	EST_HUMAN	nn01f12.x5 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.11 ORF repetitive element:
4440	9559	14701	1.01	1.0E-80	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
5111	10212	15349	1.01	1.0E-80	4557610	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
4366	9487	14630	5.13	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4366	9487	14631	5.13	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
2199	7311	12663	7.48	5.0E-81	BE288042.1	EST_HUMAN	601126505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
218	6412	10551	0.61	4.0E-81	AF262267.1	NT	Homo sapiens CRP2 binding protein mRNA, partial cds
700	5857	11005	1.37	4.0E-81	AF521435.1	EST_HUMAN	trf00e12.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85560 Q85560
1833	6956	12178	1.73	4.0E-81	AW770612.1	EST_HUMAN	hm98d02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW-COPG_BOVIN
3150	8301	13461	3.42	4.0E-81	AB037766.1	NT	P53820 COATOMER GAMMA SUBUNIT ; Homo sapiens mRNA for KIAA1345 protein, partial cds
3608	8747	13903	0.99	4.0E-81	AW004608.1	EST_HUMAN	ws90h03.x1 NCI_CGAP_Oc3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:O43815 O43815 STRIATIN ;
4132	9260	14397	2.2	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4132	9260	14398	2.2	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
1271	6400	11572	10.35	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1271	6400	11573	10.35	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2351	7458	12713	4.34	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2960	8114	13276	5.69	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA

Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2660	8114	13277	5.69	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2784	7851	13116	2.9	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2794	7851	13117	2.9	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3754	8891	14042	0.8	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2952384 3'
1431	6558	11741	1.19	1.0E-81	W26539.1	EST_HUMAN	33f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4489	9608	14746	3.07	1.0E-81	AA040370.1	EST_HUMAN	z45h09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to
4614	9732	14869	6.85	1.0E-81	BE047996.1	EST_HUMAN	PIR-S62437 S62437 CDP-diacylglycerol synthase - fruit fly;
12	5223	10335	6.68	8.0E-82	AF161406.1	NT	z45c04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2281526 5'
103	5223	10335	3.99	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
261	5451	10590	3.03	8.0E-82	U08988.1	NT	Homo sapiens HSPC288 mRNA, partial cds
815	5668	11129	2.26	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
888	6036	11209	1.2	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1501	6628	11815	1.33	8.0E-82	AB037748.1	NT	Human CRFB4 gene, partial cds
1670	6799	11995	1.21	8.0E-82	671560.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
4222	9347	14480	0.71	8.0E-82	8923432	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
1463	6590	13078	1.1	7.0E-82	BF036327.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
2728	7823	13078	1.5	7.0E-82	AU144050.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1685	6814	12012	61.3	4.0E-82	AF081484.1	NT	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
275	5485	10607	14.66	3.0E-82	4502166	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
701	5858	11006	2.26	3.0E-82	BE006706.1	EST_HUMAN	Homo sapiens amyloid beta (A4) precursor protein (precursor protein (precursor protein) (APP), mRNA
788	5942	11102	8.05	3.0E-82	5174702	NT	RC2-BN0120-010400-013-402 BN0120 Homo sapiens cDNA
871	6022	11193	8.74	3.0E-82	4502166	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
1062	6203	11673	63.03	3.0E-82	AA728948.1	EST_HUMAN	Homo sapiens amyloid beta (A4) precursor protein (precursor protein (precursor protein) (APP), mRNA
1382	6491	11673	1.14	3.0E-82	AW875073.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
1478	6606	11791	2.32	3.0E-82	AL163295.2	NT	RC6-PT0001-160100-021-B02 PT0001 Homo sapiens cDNA
1907	7026	12249	1.31	3.0E-82	BE813232.1	EST_HUMAN	Homo sapiens chromosome 21 segment H321C065
3255	8405	10884	1.94	3.0E-82	545381.1	NT	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
595	5757	10884	1.4	2.0E-82	AB023216.1	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
595	5757	10885	1.4	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
595	5757	10885	1.4	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds

Page 142 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1700	6828	12029	2.13	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117_r1 434 (synonym: htec3) Homo sapiens cDNA clone DKFZp434M117 5'
2948	8102	13267	0.7	2.0E-82	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3823	8959	14107	1	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4212	9337	14470	0.88	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4531	9849	14795	1.11	2.0E-82	AB028019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4531	9849	14796	1.11	2.0E-82	AB028019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4841	9953	15098	2.94	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSOR1) and wbscr5 (WBSOR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5084	10166	15299	1.42	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5084	10166	15300	1.42	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
590	5752	10879	1.35	1.0E-82	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1211	6343	11592	1.99	1.0E-82	BE885106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1289	6418	11592	4.73	1.0E-82	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
1290	6419	11593	1.7	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
1421	6548	11729	3.25	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5'
1695	7871	12023	2.23	8.0E-83	N66951.1	EST_HUMAN	ze48f12.s1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:296823 3'
1364	6493	11674	1.56	7.0E-83	AW385529.1	EST_HUMAN	QV4-LT0016-271289-088-h11 LT0016 Homo sapiens cDNA
2829	7984		1.62	7.0E-83	AA584655.1	EST_HUMAN	no12h07.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element
4784	9897		6.62	7.0E-83	BF221813.1	EST_HUMAN	7p37e07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316
403	5570	10717	1.49	6.0E-83	M33320.1	NT	DJ207H1.1 ; Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
1797	6922	12132	2.43	6.0E-83	AW573088.1	EST_HUMAN	h31h03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to
3023	8177		0.93	6.0E-83	AF231919.1	NT	SW:YBEB_HAEIN_P44471 HYPOTHETICAL PROTEIN H10034. ; Homo sapiens chromosome 21 unknown mRNA
3548	8889	13851	0.75	6.0E-83	11430241	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
946	6094		1.51	5.0E-83	U17983.1	NT	Homo sapiens succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2042	7875		8.24	5.0E-83	AF006305.1	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3616	8755	13911	2.15	5.0E-83	AL133207.2	NT	Novel human gene mapping to chromosome X
3983	9019	14176	1.77	5.0E-83	4885190	NT	Homo sapiens deoxyribonuclease 1 (DNASE1), mRNA
5062	10164	15297	11.94	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5062	10164	15298	11.94	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
639	5800	10934	1.69	4.0E-83	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MAN5A) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds

Page 143 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells.

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
988	6144		3.25	3.0E-83	AA368311.1	EST_HUMAN	EST79542 Placenta 1 Homo sapiens cDNA similar to endogenous retrovirus ERV9
2738	7832		1.09	3.0E-83	AA632854.1	EST_HUMAN	np87c07.s1 NCI_QCAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR.12 THR repetitive element;
1812	6935	12150	2.11	2.0E-83	AA993492.1	EST_HUMAN	cl64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216.;
1812	6935	12151	2.11	2.0E-83	AA993492.1	EST_HUMAN	cl64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216.;
1930	7049	12270	2.01	2.0E-83	N68951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
2162	7275	12522	0.97	2.0E-83	AB033098.1	NT	Homo sapiens mRNA for KIAA1272 protein, partial cds
2814	7670	13129	1.26	2.0E-83	BE828694.1	EST_HUMAN	RC6-ET0046-280600-013-H12 ET0046 Homo sapiens cDNA
3252	8402		1.97	2.0E-83	11430834	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3755	8892		0.7	2.0E-83	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4213	9435	14570	4.13	2.0E-83	AF202879.1	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4620	9738	14876	9.02	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
4620	9738	14877	9.02	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
1419	6546	11726	3.66	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1419	6546	11727	3.66	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
2617	7716	12970	4.89	1.0E-83	BE883660.1	EST_HUMAN	g01507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3608754 5'
3163	8314	13476	0.93	1.0E-83	7662349	NT	Homo sapiens cell recognition molecule Casp2 (KIA08868), mRNA
3647	8983	14138	7.16	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4223	9348	14481	2.31	1.0E-83	Z25822.1	NT	H. sapiens gene for mitochondrial dodecenoyl-CoA delta-Isomerase, exon 3
4857	9669	15114	1.56	1.0E-83	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3774	8911	14064	3.43	7.0E-84	BE901209.1	EST_HUMAN	g01676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3668853 5'
1299	6428	11600	4.09	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
1299	6428	11601	4.09	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
2374	7480	12734	3.37	6.0E-84	AA776574.1	EST_HUMAN	ae89a03.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
712	5669	11017	0.8	5.0E-84	AA382811.1	EST_HUMAN	EST98094 Testis 1 Homo sapiens cDNA 5' end
2985	8139		1.7	5.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1385	6513	11694	0.97	4.0E-84	AB037735.1	NT	Homo sapiens mRNA for KIAA1314 protein, partial cds
1418	6545	11725	3.03	4.0E-84	AI685321.1	EST_HUMAN	wa76c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN_Q43847 NARDILYSIN PRECURSOR;

Page 144 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4928	10038	15178	0.96	4.0E-84	4505928	NT	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
4929	10039	15179	1.84	4.0E-84	AF068601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5129	10229	15364	1.04	4.0E-84	AA401549.1	EST_HUMAN	zu62a07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742548 5' similar to WP:F22B5.1
314	5500	10640	1.87	3.0E-84	AF026200.1	NT	CE02185 GTP-BINDING ADP-RIBOSYLATION FACTOR
1984	7081	12305	2.9	3.0E-84	5453855	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
2006	7123	12359	7.05	3.0E-84	AL068880.1	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
3730	8867	14021	6.04	3.0E-84	AF014499.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
2096	7211	12458	3.39	2.0E-84	BE69397.1	EST_HUMAN	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRIS1) mRNA, complete cds
2096	7211	12459	3.39	2.0E-84	BE69397.1	EST_HUMAN	CM1-BT0795-190600-272-508 BT0795 Homo sapiens cDNA
2909	8083	13235	9.32	2.0E-84	AF036943.1	NT	CM1-BT0795-190600-272-508 BT0795 Homo sapiens cDNA
2931	8085	13252	1.4	2.0E-84	X89211.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1-) mRNA, complete cds
4760	9873	15024	1.01	2.0E-84	BF308518.1	EST_HUMAN	H.sapiens DNA for endogenous retroviral like element
4760	9873	15025	1.01	2.0E-84	BF308518.1	EST_HUMAN	601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'
310	5496	10636	1.31	1.0E-84	AF114488.1	NT	601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'
548	5713	10847	54.29	1.0E-84	4507952	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
718	5875	11187	1.02	1.0E-84	11427631	NT	Homo sapiens complement component 5 (C5), mRNA
1297	6426	11598	5.12	1.0E-84	AA984379.1	EST_HUMAN	am85b11.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629886 3'
2046	7162	12401	1.84	1.0E-84	BE392137.1	EST_HUMAN	601308006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626257 5'
2205	7317	12587	2.18	1.0E-84	11427197	NT	Homo sapiens pericentriolar material 1 (PCM1), mRNA
3732	8870	14023	2.48	1.0E-84	AA720851.1	EST_HUMAN	nm12806.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1289106 3'
4994	9514	14655	4.46	1.0E-84	AJ229041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4688	9784	14928	3.07	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4688	9784	14929	3.07	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4887	9514	14655	2.2	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
968	6115	11377	1.98	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1074	6214	11377	7.87	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1074	6214	11378	7.67	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1591	6720	11909	0.96	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1591	6720	11910	0.96	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1688	6817	12016	2.58	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4888	9999	15145	0.91	9.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1137	6274	11438	8.3	7.0E-85	LO5094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds

Page 145 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2314	7422	12673	1.51	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1303	6433	11607	1.63	3.0E-85	AF086157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1790	6816	12123	5.48	3.0E-85	T97495.1	EST_HUMAN	yes3g09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121504 5'
4292	9414	14549	1.03	3.0E-85	BE267189.1	EST_HUMAN	601189704F2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533616 5'
4872	9883	15129	1.55	3.0E-85	11024895	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4872	9883	15130	1.55	3.0E-85	11024895	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
964	6111	11281	0.96	2.0E-95	7657266	NT	Homo sapiens KIAA0829 protein Mix2 Interacting nuclear target (MINT) homolog (KIAA0829), mRNA
1042	6183	11349	3.03	2.0E-85	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
1412	6539	11716	1.62	2.0E-85	7706205	NT	Homo sapiens CGI-201 protein (LOC61340), mRNA
1429	6556	11738	5.07	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1429	6556	11739	5.67	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2212	7324	12674	1.75	2.0E-85	U10625.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2783	6471		6.15	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2894	8149	13309	1.39	2.0E-85	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4310	9432	14567	4.58	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4886	9997	15143	0.99	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2263	7373		2.12	1.0E-85	BE794306.1	EST_HUMAN	601591410F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'
2370	7476	12730	4.1	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
2370	7476	12731	4.1	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
1438	6665		20.94	9.0E-86	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867690 5'
937	6085	11251	0.94	7.0E-86	AA860801.1	EST_HUMAN	aj8808.s1 Soares parathyroid tumor NIHHPA Homo sapiens cDNA clone IMAGE:1403559 3'
937	6085	11252	0.94	7.0E-86	AA860801.1	EST_HUMAN	aj8808.s1 Soares parathyroid tumor NIHHPA Homo sapiens cDNA clone IMAGE:1403559 3'
1298	6427	11599	4.58	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH) mRNA
208	5402	10546	3.94	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
4285	9390	14528	0.98	3.0E-86	BE867703.1	EST_HUMAN	601443262F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3847455 5'
264	5454	10592	1.31	2.0E-86	AA306264.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
413	5681		2.4	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1192	6326	11493	1.66	2.0E-86	N58977.1	EST_HUMAN	yz18a08.r1 Soares multiple sclerosis 2NbhMSP Homo sapiens cDNA clone IMAGE:283478 5'
1505	6332	11818	1.43	2.0E-86	4758827	NT	Homo sapiens neuraxin III (NRXN3) mRNA
1505	6332	11819	1.43	2.0E-86	4758827	NT	Homo sapiens neuraxin III (NRXN3) mRNA
2174	7287	12535	1.95	2.0E-86	9635487	NT	Human endogenous retrovirus, complete genome
2249	7359	12616	3.27	2.0E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3397	8541	13700	1.44	2.0E-86	AW966142.1	EST_HUMAN	EST378215 IMAGE resequences, MAGI Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3727	8864	14017	2.82	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3727	8864	14018	2.82	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4014	9147		2.54	2.0E-86	AW515742.1	EST_HUMAN	hd87g08.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2916542 3'
4789	9869	15019	2.51	2.0E-86	AF050480.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5043	10145	15274	1.35	2.0E-86	4505778	NT	Homo sapiens phosphotyrosine kinase, alpha 1 (muscle) (PHKA1), mRNA
							Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
1610	6738	11932	2.76	1.0E-86	4826855	NT	
3141	8292	13449	1.36	1.0E-86	5453649	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3220	8371	13534	2.99	1.0E-86	L20492.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3278	8427	13588	1.25	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3278	8427	13589	1.25	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3917	9053	14213	0.99	1.0E-86	7706181	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
3917	9053	14214	0.99	1.0E-86	7706181	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4288	9363	14486	4.73	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4896	10007	15152	1.27	1.0E-86	AF100751.1	NT	Homo sapiens FK506-binding protein FKBP23 isoform mRNA, complete cds
478	5846	10787	81.05	8.0E-87	X62245.1	NT	O. cuniculus mRNA for elongation factor 1 alpha
3513	8654	13820	1.08	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
5173	10270	15411	0.63	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
1160	6266	11461	2.39	5.0E-87	AA382811.1	EST_HUMAN	EST196094 Testis 1 Homo sapiens cDNA 5' end
967	6114	11283	0.88	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1174	6309	11476	18.49	4.0E-87	AB037833.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
							y80f10.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element
1439	6566	11751	0.99	4.0E-87	R78133.1	EST_HUMAN	
2024	7141	12381	1	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
2399	7505	12753	1.48	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
2399	7605	12784	1.48	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
							Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLL14) mRNA
3446	8588	13751	1.75	4.0E-87	5174574	NT	
2737	7831	13085	5.83	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
2914	8068		0.68	2.0E-87	BF327920.1	EST_HUMAN	QV0-BN0148-050600-254-a03 BN0148 Homo sapiens cDNA
3763	8900	14052	0.78	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
4889	10000	15146	0.6	2.0E-87	BF376311.1	EST_HUMAN	GM0-TN0038-150900-552-n08 TN0038 Homo sapiens cDNA
4941	10051	15189	1.37	2.0E-87	BE175478.1	EST_HUMAN	RC5-HT0590-200300-031-G04 HT0590 Homo sapiens cDNA
1184	7869		1.7	1.0E-87	7705693	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA



Page 147 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1441	6568	11753	1.93	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141089-001-g04 CT0265 Homo sapiens cDNA
1441	6568	11754	1.93	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141089-001-g04 CT0265 Homo sapiens cDNA
3688	8827	13982	12.69	1.0E-87	Y00062.1	NT	Human mRNA for T-cell cyclophilin
3715	8853	14007	2.98	1.0E-87	4759827	NT	Homo sapiens neurexin III (NRXN3) mRNA
1107	6243	11408	6	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1366	6485	11665	2.83	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1366	6485	11666	2.83	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
2111	7226	12468	1.12	9.0E-88	7661707	NT	Homo sapiens DKFZP686P1522 protein (DKFZP686P1522), mRNA
3607	8746	13902	1.03	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4243	9368	14501	3.03	9.0E-88	X91826.1	NT	H. sapiens ECE-1 gene (exon 9)
4243	9368	14502	3.03	9.0E-88	X91929.1	NT	H. sapiens ECE-1 gene (exon 9)
4989	10095	15226	1.01	9.0E-88	AB028698.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1842	6963		2.34	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2603	7702	12959	9.44	5.0E-88	N88399.1	EST_HUMAN	K9718F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
2970	8124	13287	0.68	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
2982	8136	13300	0.63	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
2982	8136	13301	0.63	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3370	8515		2.52	5.0E-88	AI693217.1	EST_HUMAN	wd88h08.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu repetitive element; contains element MER22
3523	8634	13831	0.87	5.0E-88	AF114488.1	NT	repetitive element; contains element MER22 repetitive element ;
4705	9821	14968	0.62	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
1334	6463	11643	1.8	4.0E-88	BF091229.1	EST_HUMAN	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
1334	6463	11644	1.8	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
730	5886	11036	2.2	3.0E-88	11545800	NT	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
1824	6947		1.79	3.0E-88	4508020	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
2913	8067	13240	4.81	3.0E-88	N66951.1	EST_HUMAN	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
4219	9344	14474	0.66	3.0E-88	4501912	NT	z48f12.61 Scarsa fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:295823 3'
4219	9344	14475	0.66	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4457	9676		3.97	3.0E-88	11429300	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
1036	6179	11343	1.32	2.0E-88	7305198	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
1636	6765	11959	1.88	2.0E-88	AF246219.1	NT	Homo sapiens Calsenilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1762	6888	12094	4.8	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4403	9523	14664	1.99	2.0E-88	5031666	NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA
2697	7793	13044	1.51	8.0E-89	BE311557.1	EST_HUMAN	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5'
432	5601	10747	1.21	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
432	5601	10748	1.21	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
4853	9665	15110	3.03	7.0E-89	4557390	NT	Homo sapiens complement component 8, beta polypeptide (C8B), mRNA
4908	10018	15162	3.96	7.0E-89	AL045748.1	EST_HUMAN	DKFZp434E246_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E246 5'
1024	6165	11331	1.25	6.0E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
2195	7307	12557	4.18	6.0E-89	4506124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4), mRNA
2411	7517	12766	3.33	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA
2411	7517	12767	3.33	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA
3511	8652	13818	1.12	6.0E-89	7661817	NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4607	9725	14860	3.88	6.0E-89	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4607	9725	14861	3.88	6.0E-89	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5148	10248	15386	0.69	6.0E-89	6809918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5148	10248	15387	0.69	6.0E-89	6809918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5058	10160	15292	3	6.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5058	10160	15293	3	6.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
2842	7997	13155	1.58	3.0E-89	AW976181.1	EST_HUMAN	EST388290 IMAGE resequences, MAGN Homo sapiens cDNA
122	5575	10723	0.76	2.0E-89	7705670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
122	5575	10724	0.76	2.0E-89	7705670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
528	5594	10826	0.67	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2847	8002	13162	1.46	2.0E-89	AI222095.1	EST_HUMAN	q996c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131
4116	9244	14380	1.49	2.0E-89	AF089897.1	NT	GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
4125	9253	14391	5.06	2.0E-89	X58742.1	NT	Homo sapiens topoisomerase-related function protein (TRF4.2) mRNA, partial cds
4125	9253	14392	5.06	2.0E-89	X58742.1	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4125	9448	14581	1.08	2.0E-89	AL163203.2	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4474	9593	14732	1.18	2.0E-89	AJ007378.1	NT	Homo sapiens chromosome 21 segment HS21C003
1064	6205	11367	3.39	8.0E-90	AL163246.2	NT	Homo sapiens GGT gene, exon 5
1065	6205	11367	3.2	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1335	7914	11645	6.99	8.0E-90	BE670561.1	EST_HUMAN	7636108.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1335	7914	11646	6.99	8.0E-90	BE670561.1	EST_HUMAN	7c36f08.x1 NCI_GGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
837	5989		7	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3040	8194	13349	1.25	6.0E-90	X91926.1	NT	H.sapiens ECE-1 gene (exon 6)
3040	8194	13350	1.25	6.0E-90	X91926.1	NT	H.sapiens ECE-1 gene (exon 6)
4204	8329	14461	7.5	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4204	9329	14462	7.5	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
150	5347		33.35	5.0E-90	AB035344.1	NT	Homo sapiens TCL6 gene, exon 4-10b
1195	6329	11496	3.1	5.0E-90	U80228.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1831	6954	12176	1.4	6.0E-90	A1222095.1	EST_HUMAN	qg96c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL-TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
1831	6954	12176	1.41	5.0E-90	A1222095.1	EST_HUMAN	qg96c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL-TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
2525	7628	12875	1.38	5.0E-90	AF114487.1	NT	Homo sapiens Intersectin long isoform (ITSN) mRNA, complete cds
4513	9631	14776	0.96	6.0E-90	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4641	9759	14906	0.66	5.0E-90	AL135549.1	EST_HUMAN	DKFZp762P1616_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762P1616 5'
300	5488	10629	2.48	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
300	5488	10630	2.48	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1087	6226	11391	3.88	4.0E-90	4506316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1703	6831	12033	8.69	4.0E-90	X90033.1	NT	H.sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
2824	7980	13140	0.63	4.0E-90	6906918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2824	7980	13141	0.63	4.0E-90	6906918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2995	8150	13310	1.03	4.0E-90	6906918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2995	8150	13311	1.03	4.0E-90	6906918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4626	9744	14888	5.2	4.0E-90	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4766	9879	15028	2.32	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4787	9900	15041	1.98	4.0E-90	M95967.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 8
211	5405	10548	3	2.0E-90	BE537913.1	EST_HUMAN	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1175	6310	11477	23.99	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1175	6310	11478	23.99	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3822	8958	14108	1.81	2.0E-90	A1139213.1	EST_HUMAN	qc54c02.x1 Scores_placenta_8t69weeks_2NhrP8t69W Homo sapiens cDNA clone IMAGE:17134410 3' similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3.;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4885	9956	15142	7.01	2.0E-90	5729855	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
274	5464	10606	4.6	1.0E-90	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
372	7863	10695	3.01	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
373	7863	10695	2.12	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
693	5850	10984	1.7	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBOX2 gene), partial
693	5850	10995	1.7	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBOX2 gene), partial
728	5884	11033	12.93	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
728	5884	11034	12.93	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1111	6249		4.98	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1310	6440	11618	2.9	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1310	6440	11617	2.9	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1681	6810		5.61	1.0E-90	BE379884.1	EST_HUMAN	901159563F2 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:361118 5'
1908	7027	12247	2.4	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA
2816	7972	13132	6.74	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (G8ORF2), mRNA
3830	8966	14118	0.95	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3830	8966	14119	0.95	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
							Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
4401	9521	14662	1.31	1.0E-90	AF167340.1	NT	HUM000S381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'
4168	9294	14432	5.3	8.0E-91	D12234.1	EST_HUMAN	Rattus norvegicus brain specific cortactin-binding protein CBF90 mRNA, partial cds
1457	6584	11772	1.01	7.0E-91	AF063768.1	NT	250b04.s1 Soares_fetal_liver_spleen_1NF15_S1 Homo sapiens cDNA clone IMAGE:448015 3'
3436	8398	13762	2.08	5.0E-91	AA702794.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4490	9609	14747	1.1	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4490	9609	14748	1.1	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4777	9880	15035	1.24	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4777	9880	15036	1.24	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
3185	8336	13498	11.3	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3185	8336	13499	11.3	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
1629	6758	11952	2.26	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1629	6758	11953	2.26	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1802	7572	12140	1.36	3.0E-91	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
3321	8468	13631	1.48	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3444	8586	13748	2.96	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3444	8586	13749	2.96	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds

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3767	8904	14057	2.23	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4564	9082	14821	3.8	3.0E-91	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4984	10072	15209	1.05	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4984	10072	15210	1.05	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
47	5259	10383	3.17	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1249	6379	11558	9.53	1.0E-91	AW449746.1	EST_HUMAN	UI-H-B13-aks-Q-01-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
1245	6376	11552	10.34	9.0E-92	AJ001689.1	NT	Homo sapiens NKX2D gene, exon 10
1245	6376	11553	10.34	9.0E-92	AJ001689.1	NT	Homo sapiens NKX2D gene, exon 10
88	5297	10436	5.9	8.0E-92	W26367.1	EST_HUMAN	28f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
283	5472	10514	6.45	8.0E-92	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3614667 5'
5085	10185	15323	1.03	8.0E-92	AW157574.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to
234	7886	10566	1.01	7.0E-92	AB018301.1	NT	TR:O60302 O60302 KIAA0555 PROTEIN, contains element MER22 repetitive element ;
234	7886	10567	1.01	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
589	5751	1	1	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Septase truncated isoform mRNA, complete cds
1284	6413	11689	2.65	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2169	7282	12528	10.41	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2169	7282	12529	10.41	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2533	7636	12884	1.27	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2887	7784	13032	10.39	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
2716	7811	13066	1.19	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3327	10306	13635	0.75	7.0E-92	4607500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3327	10306	13636	0.75	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4561	9879	14818	1.17	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4561	9879	14819	1.17	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
1800	6728		1.37	5.0E-92	BE390882.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605018 5'
2727	7622	13077	3.98	3.0E-92	BE909714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902939 5'
24	5235	10349	1.34	2.0E-92	4501988	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
174	5368	10508	3.34	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA
174	5368	10509	3.34	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA
748	5804	11059	4.61	2.0E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
748	5804	11060	4.61	2.0E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1729	6856		1.9	2.0E-92	S76653.1	NT	mRNAs-related [human, Genomic, 2416 nt]
1940	7059	12281	2.6	2.0E-92	AI818119.1	EST_HUMAN	wk27d07.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
1940	7059	12282	2.6	2.0E-92	AI818119.1	EST_HUMAN	wk27d07.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
1967	7084	12309	1.97	2.0E-92	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1967	7084	12310	1.97	2.0E-92	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
2040	7157	12397	7.53	2.0E-92	4506860	NT	Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA
2620	7719	12973	1.4	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2790	6793	11992	1.09	2.0E-92	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2790	6793	11993	1.09	2.0E-92	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3597	8736	13688	1.18	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3597	8736	13689	1.18	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3663	8802	13958	6.99	2.0E-92	5803180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4263	9368	14525	1.72	2.0E-92	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
4979	10087		2.29	2.0E-92	AL040437.1	EST_HUMAN	DKFZp434C0414_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0414 5'
1861	6981	12204	1.77	1.0E-92	R78078.1	EST_HUMAN	y80a08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
1861	6981	12205	1.77	1.0E-92	R78078.1	EST_HUMAN	y80a08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
2065	7181	12421	63.38	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
2022	7139	12379	2.17	9.0E-93	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
2036	7154		26.69	9.0E-93	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4312	9434	14569	1.42	9.0E-93	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
243	5434	10573	6.55	7.0E-93	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3047	8201	13357	0.67	6.0E-93	11528176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
1391	6519	11689	4.35	5.0E-93	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1415	6542	11720	13.82	5.0E-93	AI674184.1	EST_HUMAN	wc09c08.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3'
1415	6542	11721	13.82	5.0E-93	AI674184.1	EST_HUMAN	wc09c08.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3'
1835	7927	12180	1.01	5.0E-93	AI297710.1	NT	Homo sapiens mRNA for GDC2L5 protein kinase, (GDC2L5 gene), isoform 2
3218	8369	13532	4.95	5.0E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
83	5292		4.53	4.0E-93	AA455933.1	EST_HUMAN	z60a09.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to SW:GLPA_RAT
444	5612	10757	1.44	4.0E-93	4557879	NT	P37397 CALPONIN, ACIDIC (ISOFORM ; Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA

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444	5912	10768	1.44	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
772	5928	11084	2.86	4.0E-93	7857454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PEST), mRNA
772	5926	11085	2.86	4.0E-93	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PEST), mRNA
1186	6310	11487	1.84	4.0E-93	8923658	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
1979	7086	12327	2.62	4.0E-93	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in Intron 5
2225	7337	12591	1.18	4.0E-93	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
2376	7481	12735	1.31	4.0E-93	AL183301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3553	8694	13856	0.85	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
4022	9154	14268	1.47	4.0E-93	4504654	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
5008	8984	13856	0.85	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
3629	8768	13923	9.7	3.0E-93	BF690630.1	EST_HUMAN	602246954F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
3629	8768	13924	9.7	3.0E-93	BF690630.1	EST_HUMAN	602246954F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
5052	10154		0.94	3.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
187	5382	10523	26.53	2.0E-93	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
187	5382	10524	26.53	2.0E-93	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
321	5507	10646	13.27	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
322	5507	10646	5.79	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2121	7236	12479	2.73	2.0E-93	U40763.1	NT	Human Cdk-associated RS cyclophilin CAPS-Cyp mRNA, complete cds
2461	7565	12818	1.71	2.0E-93	BE252982.1	EST_HUMAN	60117589F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
99	5308	10447	2.56	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
99	5308	10448	2.56	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
516	5882	10816	18.65	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (DJ328E18.C1.1), mRNA
598	5760	10888	3.83	1.0E-93	AI146755.1	EST_HUMAN	0784608 x1 NCL CGAP_CELL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q82384 Q82384
873	6024	11195	7.53	1.0E-93	D87676.1	NT	ZINC FINGER PROTEIN, ;
1240	6370	11543	9.84	1.0E-93	8923270	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1240	6370	11544	9.84	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1350	6479	11658	1.17	1.0E-93	AB046783.1	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1352	6481	11650	1.18	1.0E-93	AF167706.1	NT	Homo sapiens mRNA for KIAA1563 protein, partial cds
2319	7427	12679	5.52	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2440	7544	12798	1.52	1.0E-93	AF05066.1	NT	Homo sapiens MHC class 1 region
2477	7582		1.11	1.0E-93	AL137200.1	NT	Novel human gene mapping to chromosome 1

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2782	8429	11602	2.88	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2782	8429	11603	2.88	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2899	8053	13222	3.67	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3201	8352		1.55	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4407	9527	14687	1.98	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3935	9071	14227	1.85	6.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
1854	6975		21.15	4.0E-94	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2618	7717	12971	1.78	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3649	8789	13942	1.02	4.0E-94	AW197851.1	EST_HUMAN	xr89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3649	8788	13943	1.02	4.0E-94	AW197851.1	EST_HUMAN	xr89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4085	9801	14947	2.97	4.0E-94	AI591312.1	EST_HUMAN	hw11f10.x1 NCL CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15265
608	5768	10897	3.14	3.0E-94	AB022785.1	NT	PROTEIN TYROSINE PHOSPHATASE ;
719	5876	11023	1.3	3.0E-94	4502506	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
1751	8877	12082	1.29	3.0E-94	AF167708.1	NT	Homo sapiens complement component 5 (C5) mRNA
1751	8877	12083	1.29	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1782	6909	12116	2.04	3.0E-94	4557556	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
4160	9286	14421	0.7	3.0E-94	AA464805.1	EST_HUMAN	Homo sapiens E1A binding protein p300 (EP300) mRNA
144	5341	10485	3.43	1.0E-94	BE295714.1	EST_HUMAN	zw63g08.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:774782 5'
3061	8214	13387	2.73	1.0E-94	BE293433.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3061	8214	13388	2.13	1.0E-94	BE253133.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4336	9458	14596	0.99	1.0E-94	9506692	NT	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4757	9870	15020	4.78	1.0E-94	AI904151.1	EST_HUMAN	Homo sapiens hypothetical protein (FLJ20746), mRNA
1487	6614	11802	2.81	9.0E-95	AF027302.1	NT	CMA-BT043-080298-075 BT043 Homo sapiens cDNA
3134	8285	13441	1.02	9.0E-95	7662027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3134	8285	13442	1.02	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
4509	9628	14771	1.81	8.0E-95	AI700698.1	EST_HUMAN	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
4509	9628	14772	1.81	8.0E-95	AI700698.1	EST_HUMAN	we09e04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00556
273	5463	10604	12.32	7.0E-95	D87675.1	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
273	5463	10605	12.32	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4345	9467	14605	4.62	7.0E-95	M95708.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
							Homo sapiens Lys-like protein (CD59) mRNA, complete cds



Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4391	6511		1.35	7.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1656	6784	11977	4.12	2.0E-05	7692027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1656	6784	11978	4.12	2.0E-05	7692027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1946	7063	12287	1.73	2.0E-05	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA
1948	7068	12291	2.79	2.0E-05	BE393873.1	EST_HUMAN	801312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3688862 5'
2403	7509	12758	1.47	2.0E-05	5453685	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2403	7509	12759	1.47	2.0E-05	5453685	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2442	7546	12799	1.77	2.0E-05	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2484	7698	12837	2.67	2.0E-05	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
3136	8297	13444	2.59	2.0E-06	AF016482.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3550	8691	13832	2.81	2.0E-05	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3550	8691	13853	2.81	2.0E-05	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3600	8739	13892	2.18	2.0E-05	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
3731	8869	14022	3.84	2.0E-05	A1280264.1	EST_HUMAN	qm01c02.x1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:123G7.4
4339	9461	14598	1.62	2.0E-05	7657185	NT	CE03705;
5021	10123	15255	2.79	2.0E-05	7661979	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
441	7890	10754	1.39	8.0E-06	BE907607.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
441	7890	10755	1.39	8.0E-06	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
3880	8022	14179	1.23	7.0E-06	AF231920.1	NT	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
2240	7351	12608	3.03	6.0E-06	BE171984.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3299	8446	13608	0.92	6.0E-06	AL163201.2	NT	MR0-HT0559-250200-002-d07 HT0559 Homo sapiens cDNA
3484	8608	13770	38.5	6.0E-06	M26873.1	NT	Homo sapiens chromosome 21 segment HS21C001
5190	10287	15423	1.28	6.0E-06	A1423283.1	EST_HUMAN	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3' end
318	5504	10842	2.15	5.0E-06	AB032998.1	NT	{f41d03.x1 NCI_CGAP_Brr23 Homo sapiens cDNA clone IMAGE:2098757 3'
843	5994	11163	3.36	5.0E-06	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
843	5994	11164	3.36	5.0E-06	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2583	7694		2.51	5.0E-06	X60812.1	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
4877	9988		1.63	5.0E-06	X60812.1	NT	H. sapiens DNA for monamine oxidase type A (7) (partial)
5160	10250	15389	0.56	5.0E-06	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
4192	9298		8.24	3.0E-06	H68656.1	EST_HUMAN	Y87H12.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212327 5'
414	5592		3.71	2.0E-06	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA

Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
746	5902	11056	1.52	2.0E-96	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1804	6928	12142	1.43	2.0E-96	7706205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
4723	9837	14981	1.05	2.0E-96	BE148074.1	EST_HUMAN	RC3-H10230-040500-110-g02.H10230 Homo sapiens cDNA
620	5780	10909	2.02	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
620	5780	10910	2.02	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
670	5829	10969	5.56	1.0E-96	Y18990.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1791	6917	12124	8.41	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
1791	6917	12125	8.41	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
2246	7876	12614	1.72	1.0E-96	U51472.2	NT	Felis catus superfast myosin heavy chain (sMyHC) mRNA, complete cds
3308	8455	13617	0.99	6.0E-97	BF245240.1	EST_HUMAN	601863712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202.6
939	6087	11255	3.71	4.0E-97	BE004436.1	EST_HUMAN	CMD-BN0106-170300-293-a08 BN0106 Homo sapiens cDNA
949	6097	11265	1.34	4.0E-97	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
949	6097	11266	1.34	4.0E-97	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
1914	7033	12253	4.55	4.0E-97	5453572	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
240	5432	10571	2.11	3.0E-97	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
876	6026	11197	14.13	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
876	6026	11198	14.13	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1452	7918	11768	1.45	3.0E-97	4758813	NT	Homo sapiens N-myc (and STAT) Interactor (NMI), mRNA
2416	7877	12772	2.12	3.0E-97	U36266.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 7
3243	8393	13955	0.99	3.0E-97	5174478	NT	Homo sapiens pericentriin (PCNT) mRNA
4747	9860	15009	26	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
902	6052	11222	6.13	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1280	8409	11584	1.08	9.0E-98	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
4845	9763		1.26	9.0E-98	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1381	6609	11690	1.09	8.0E-98	AB033768.1	NT	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
1575	6703	11892	1.32	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1575	6703	11893	1.32	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1739	6866	12070	5.86	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1739	6866	12071	5.86	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3773	8910	14063	6.28	8.0E-98	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
2158	7271	12519	1.29	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone IB
2572	7672	12927	2.89	3.0E-98	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2712	7807		3.52	3.0E-08	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
734	5890	11042	1.37	2.0E-08	BE281694.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'
2071	7187	12428	2.46	2.0E-08	BE294281.1	EST_HUMAN	601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3628134 5'
2219	7331	12584	3.31	2.0E-08	AL183202.2	NT	Homo sapiens chromosome 21 segment HS21C002
3109	8282	13416	1	2.0E-08	AB032377.1	NT	Homo sapiens hCHK1 gene for checkpoint kinase, exon 2
3109	8282	13417	1	2.0E-08	AB032377.1	NT	Homo sapiens hCHK1 gene for checkpoint kinase, exon 2
4081	9210	14347	1.2	2.0E-08	8923308	NT	Homo sapiens hypothetical protein FLJ20333 (FLJ20333), mRNA
4272	9396	14535	0.69	2.0E-08	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4317	9439	14572	3.11	2.0E-08	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FAACL4) mRNA
4795	9908	15047	1.63	2.0E-08	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
4795	9908	15048	1.63	2.0E-08	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
5122	10223	15357	0.96	2.0E-08	AI200657.1	EST_HUMAN	q62f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1764633 3' similar to SW:CYT_COTJA
5122	10223	15358	0.96	2.0E-08	AI200657.1	EST_HUMAN	P81061 CYSTATIN ;
405	5572	10720	80.3	1.0E-08	AI882007.1	EST_HUMAN	q62f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1764633 3' similar to SW:CYT_COTJA
454	5622	10765	3.16	1.0E-08	AW698611.1	EST_HUMAN	tw36b04.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL28_HUMAN
1809	6092	12147	55.14	1.0E-08	N49818.1	EST_HUMAN	P29316 60S RIBOSOMAL PROTEIN L23A ;
471	6638	10780	0.64	6.0E-09	U10991.1	NT	PMO-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA
3865	9001	14159	1.57	6.0E-09	AW076364.1	EST_HUMAN	y23f05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243565 5' similar to
4713	9829	14972	1.06	6.0E-09	4502680	NT	PIR:S54204 S54204 ribosomal protein L29 - human ;
920	6099	11234	0.63	5.0E-09	U35484.1	NT	Human G2 protein mRNA, partial cds
920	6099	11235	0.63	5.0E-09	U35484.1	NT	Human G2 protein mRNA, partial cds
1988	7085	12311	1.27	5.0E-09	Y11365.1	NT	Human protein G inhibitor (PGI-B) mRNA, complete cds
4537	9655	14800	2.03	5.0E-09	AF008880.1	NT	Human protein G inhibitor (PGI-B) mRNA, complete cds
4694	9810	14957	1.06	5.0E-09	AF265555.1	NT	H.sapiens IMPA gene, exon 8
4694	9810	14958	1.06	5.0E-09	AF265555.1	NT	Homo sapiens T cell receptor beta locus, TORBV/S342 to TORBV/252 region
1243	8374		26.56	2.0E-09	AW274792.1	EST_HUMAN	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
3242	8392	13554	1.48	2.0E-09	M30938.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
4516	9834	14779	1.05	2.0E-09	AF095703.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
							xc09a06.x1 NCI CGAP_HJN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN
							LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
							Human Ku (p70/p80) subunit mRNA, complete cds
							Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene
							encoding mitochondrial protein, complete cds

Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
313	5499	10839	1.14	1.0E-99	AF114487.1	NT	Homo sapiens Intersectin long isoform (ITSN) mRNA, complete cds
377	5555	10899	1.28	1.0E-99	11528150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
1430	6557	11740	5.38	1.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1571	6599	11886	2.04	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1571	6599	11887	2.04	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1932	7051	12272	1.04	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 8 (38kD) (FKBP8) mRNA, and translated products
1932	7051	12273	1.04	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 8 (38kD) (FKBP8) mRNA, and translated products
3057	8210	13364	0.94	1.0E-99	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4359	9481	14619	2.23	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4359	9481	14620	2.23	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
1	5214	10326	1.7	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	5214	10326	2.2	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
67	5277	10411	1.08	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XXRY), mRNA
67	5277	10412	1.08	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XXRY), mRNA
164	5360	10500	0.86	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
315	5501	10841	1.29	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
341	5524	10860	2.31	1.0E-100	T05087.1	EST_HUMAN	EST02975 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBGR32
436	5605		1.62	1.0E-100	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
489	5657		10.45	1.0E-100	X99631.1	NT	G.gorilla DNA for ZNF80 gene homolog
509	5675	10809	1.96	1.0E-100	BE180606.1	EST_HUMAN	RC3-HIT0675-040500-022-b09 HT0625 Homo sapiens cDNA
1020	6161	11326	2.55	1.0E-100	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1020	6161	11327	2.55	1.0E-100	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1446	6574	11760	1.25	1.0E-100	BF530735.1	EST_HUMAN	S02072064F1 NCI CGAP_Bri87 Homo sapiens cDNA clone IMAGE:4215039 5'
1561	6890		1.33	1.0E-100	AW207555.1	EST_HUMAN	U1-H-B11-afk-c-07-0-J1 st NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1568	6894	11881	1.14	1.0E-100	A1200857.1	EST_HUMAN	q162109.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1754833 3' similar to SW:CYT_COTJA
1875	6995	12220	1.36	1.0E-100	AB032894.1	NT	P81061 CYSTATIN1
2415	7521	12771	1.03	1.0E-100	X02408.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2668	7764	13015	1.76	1.0E-100	11418976	NT	H. sapiens mRNA for IFN-gamma (pKC-0)
2930	8145		3.49	1.0E-100	D11078.1	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
4183	9309	14446	1.33	1.0E-100	AF057354.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4214	9339	14471	2.03	1.0E-100	4503792	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
5076	10177	15311	3.28	1.0E-100	5032104	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
							Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5076	10177	15312	3.28	1.0E-100	6032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
76	5285	10424	1.2	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
76	5285	10425	1.2	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
684	5842	10981	2.66	1.0E-101	A8007915.2	NT	Homo sapiens mRNA for KIAA0446 protein, partial cds
702	5859	11007	5.55	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
702	5859	11008	5.55	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
771	5925	11083	3.3	1.0E-101	7657454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
854	6005	11178	1.67	1.0E-101	4503914	NT	Homo sapiens phosphoribosylaminimidazole synthetase (GART) mRNA
926	6074	11242	0.74	1.0E-101	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
986	6132	11303	17.11	1.0E-101	BF681218.1	EST_HUMAN	602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297291 5'
1054	6195	11359	2.32	1.0E-101	A1221878.1	EST_HUMAN	qg9e09.x1 Soares_NFL_I_G8C_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
1596	6725	11917	1.18	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1598	6725	11918	1.18	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1758	6884	12091	1.22	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1758	6884	12092	1.22	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1949	7067	12292	1.42	1.0E-101	4502886	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
2048	7164	12403	3.43	1.0E-101	BE843070.1	EST_HUMAN	RC3-ST0281-160500-018-H09 ST0281 Homo sapiens cDNA
2329	7938	12889	1.77	1.0E-101	5729892	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2579	7680	12935	5.25	1.0E-101	X72993.1	NT	H. sapiens EWS gene, exon 6
2706	7801	13053	3	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2706	7801	13054	3	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2922	8076		12.48	1.0E-101	AJ252312.1	NT	Homo sapiens genomic downstream Rhesus box
3186	8337	13500	2.75	1.0E-101	4885270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3225	8375		2.36	1.0E-101	BF036327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3892086 5'
3362	8507	13674	1.86	1.0E-101	AW965559.1	EST_HUMAN	EST377629 MAGE resequences, MAGI Homo sapiens cDNA
3381	7801	13053	1.65	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3381	7801	13054	1.65	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3683	8822	13978	0.74	1.0E-101	AF079299.1	NT	Homo sapiens Na+/H+ exchanger isoform 2 (NHE2) mRNA, complete cds
3854	8900	14146	4.59	1.0E-101	AB022785.1	NT	Homo sapiens Ash2L gene, complete cds, similar to Drosophila ash2 gene
5017	10119	15262	1.61	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5017	10119	15263	1.61	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
38	5249	10367	1.36	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
339	5522	10657	5.21	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
617	5777	10908	1.27	1.0E-102	BE252470.1	EST_HUMAN	B01108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
775	5929	11088	0.98	1.0E-102	4557534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1118	6256	11420	5.62	1.0E-102	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1272	6401	11574	1.69	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1272	6401	11575	1.69	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1427	6554	11738	490.48	1.0E-102	BE408447.1	EST_HUMAN	B01289882F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5'
2266	7395	12646	4.12	1.0E-102	A1124689.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95 HUMAN Q08379 GOLGIN-95;
2266	7395	12647	4.12	1.0E-102	A1124689.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95 HUMAN Q08379 GOLGIN-95;
2822	7978	13137	0.7	1.0E-102	11419442	NT	Homo sapiens peroxisome biogenesis factor 1 (PEX1), mRNA
2997	8152	13347	0.78	1.0E-102	Y13932.1	NT	Homo sapiens PRKY exon 7
3037	8191	13347	1.83	1.0E-102	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3111	8264	13418	5.67	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3111	8264	13419	5.67	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4210	8335	14467	1.54	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4389	9509	14651	1.93	1.0E-102	BE251310.1	EST_HUMAN	B01107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343982 5'
5097	10197	15335	1.04	1.0E-102	R66488.1	EST_HUMAN	y32c04.r1 Soares placenta N62HP Homo sapiens cDNA clone IMAGE:140934 5'
68	5278	10413	2.08	1.0E-103	BE908156.1	EST_HUMAN	B01500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
68	5278	10414	2.08	1.0E-103	BE908156.1	EST_HUMAN	B01500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
96	5306	10444	6.79	1.0E-103	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
205	5400	10542	3.51	1.0E-103	6463703	NT	Homo sapiens nuclear protein (KKEID repeat) (NOP56) mRNA
982	6128	11296	0.84	1.0E-103	AJ276348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1247	6377	11556	6.89	1.0E-103	BE877541.1	EST_HUMAN	B01485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887878 5'
1609	6737	11931	3.26	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1917	7036	12256	1.53	1.0E-103	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
1977	7094	12323	0.99	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1977	7094	12324	0.99	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2281	7391	12642	4.9	1.0E-103	AU134991.1	EST_HUMAN	AU134991 PLACE4 Homo sapiens cDNA clone PLACE1000665 5'
2427	7531	12784	1.1	1.0E-103	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2584	7685	12939	1.87	1.0E-103	N32770.1	EST_HUMAN	w691d08.s1 Soares placenta 8to9weeks_2NbhP8to9w Homo sapiens cDNA clone IMAGE:259599 3'
3041	8195		2.84	1.0E-103	BE744722.1	EST_HUMAN	B01573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
3381	8506	13673	3.62	1.0E-103	AW288245.1	EST_HUMAN	UIH-BW0-q1h-11-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3'

Page 161 of 214

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3421	8553	13720	0.97	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3735	8873		14.94	1.0E-103	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3771	8808	14061	1.86	1.0E-103	AA485663.1	EST_HUMAN	ab10d12.s1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element
3808	8945	14094	1.88	1.0E-103	11430876	NT	Homo sapiens neurophilin 1 (NRP1), mRNA
3978	9112	14280	2.69	1.0E-103	T23683.1	EST_HUMAN	seq340 b4HB3MA-Cot109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-7 3'
232	5428	10564	4.96	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072.1 564 (synonym: hbr2) Homo sapiens cDNA clone DKFZp564H1072 5'
232	5426	10565	4.96	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072.1 564 (synonym: hbr2) Homo sapiens cDNA clone DKFZp564H1072 5'
1896	7015	12235	1.59	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8), mRNA
2177	7290	12537	7.35	1.0E-104	AA132975.1	EST_HUMAN	zo22c06.s1 Stratiogene lung (#937204) Homo sapiens cDNA clone IMAGE:587626 3' similar to gb:714116.maf1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2187	7299	12548	5.57	1.0E-104	BE744028.1	EST_HUMAN	801577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5'
2349	7458	12710	1.14	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA
2349	7456	12711	1.14	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA
2414	7520	12770	7.5	1.0E-104	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2473	7577	12828	2.1	1.0E-104	7862125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2473	7577	12829	2.1	1.0E-104	7862125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2835	7990	13150	7.41	1.0E-104	M34871.1	NT	Human lymphocyte antigen CD59/MEM43 mRNA, complete cds
2882	8036		2.55	1.0E-104	Y11151.1	NT	Human lymphocyte antigen CD59/MEM43 mRNA, complete cds
3246	8396	13558	1.02	1.0E-104	AU133926	EST_HUMAN	H.sapiens gene encoding phenylpyruvate tautomerase II
3372	8517		2.01	1.0E-104	AU133926	EST_HUMAN	AU133926 OVARC1 Homo sapiens cDNA clone OVARC1000936 5'
3914	9060	14209	1.03	1.0E-104	AB032998.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
4101	9230	14367	0.77	1.0E-104	F11745.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4356	9478	14616	3.84	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4581	9699	14836	2.16	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4581	9699	14837	2.16	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
276	7961	10608	4.52	1.0E-105	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
424	5211	10323	39.86	1.0E-105	4505150	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
592	5754	10881	3.76	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
592	5754	10882	3.76	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1893	6822		2.63	1.0E-105	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
1832	6955	12177	0.99	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1931	7050	12271	1.54	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds

Single Exon Probes Expressed in BT474

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2172	7285	12533	55.09	1.0E-105	AA318369.1	EST_HUMAN	EST20609 Spleen   Homo sapiens cDNA 5' end similar to autolysosomal antigen Ku, p70/p80 subunit
2302	7411		1.11	1.0E-105	BE891766.1	EST_HUMAN	601434491F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919511 5'
2683	7780		1.32	1.0E-105	AA584808.1	EST_HUMAN	no10c05.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100265 3'
2978	8132		2.98	1.0E-105	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and GBR1 on chromosome 21q22; segment 1/3
3333	8479	13844	0.87	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3333	8479	13845	0.87	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4073	9203	14339	2.78	1.0E-105	AW661888.1	EST_HUMAN	EST373761 MAGE resequences, MAGG Homo sapiens cDNA
4916	10026		4.61	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5089	10189	15329	0.91	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5130	10230	15365	1.44	1.0E-105	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
146	5343		2.75	1.0E-106	AW503208.1	EST_HUMAN	U1-HF-BN0-akt-g-07-0-U1.7 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
202	5397	10540	1.83	1.0E-106	AI565065.1	EST_HUMAN	tg79607.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2215008 3'
540	5706	10840	1.77	1.0E-106	AW965596.1	EST_HUMAN	EST377629 MAGE resequences, MAG1 Homo sapiens cDNA
602	5784	10892	1.69	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (pst-hd1)
603	5784	10892	2.18	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (pst-hd1)
1538	6666	11852	1.63	1.0E-106	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1716	6843	12046	3.28	1.0E-106	U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1815	6938	12154	2.46	1.0E-106	AA527446.1	EST_HUMAN	ng41c05.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:937362 3' similar to contains element LTR3 repetitive element
1815	6938	12155	2.46	1.0E-106	AA527446.1	EST_HUMAN	ng41c05.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:937362 3' similar to contains element LTR3 repetitive element
2114	7229	12471	1.66	1.0E-106	BE144286.1	EST_HUMAN	MRO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2295	7404	12656	12.07	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2475	7579	12831	1	1.0E-106	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2565	7666	12921	1.38	1.0E-106	UB4675.2	NT	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2567	7668	12923	1.3	1.0E-106	BE260201.1	EST_HUMAN	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5'
2721	7816	13072	9.55	1.0E-106	AJ278628.1	EST_HUMAN	qj76h10.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'
2785	6569	11755	2.61	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2785	6569	11756	2.61	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2840	7995	13153	1.51	1.0E-106	BE384298.1	EST_HUMAN	601272875F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613818 5'
2807	8080	13230	4.79	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
2907	8060	13231	4.79	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3160	8311	13471	3.81	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA



Table 4

## Single Exon Probes Expressed in BT474

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3160	8311	13472	3.81	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3355	8500	13668	0.77	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3422	8564	13721	1.06	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3422	8564	13722	1.06	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4012	9145	14285	7.75	1.0E-106	AW974650.1	EST_HUMAN	EST368875 IMAGE resequences, MAGN Homo sapiens cDNA
4012	9145	14286	7.75	1.0E-106	AW974650.1	EST_HUMAN	EST368875 IMAGE resequences, MAGN Homo sapiens cDNA
4031	9162	14304	1.26	1.0E-106	6729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
4471	9590	14730	1.29	1.0E-106	AA625526.1	EST_HUMAN	af7267.r1 Soares_NH-MP_u_S1 Homo sapiens cDNA clone IMAGE:1047689 5'
4574	9692	14829	1.05	1.0E-106	BE144286.1	EST_HUMAN	MRO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
233	5427		3.11	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
282	5452		1.86	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
619	5779		4.12	1.0E-107	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
629	5789	10922	2.1	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
814	5967	11128	2	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
887	6037	11208	2.66	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
970	6117	11286	10.71	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1282	6411	11587	2.27	1.0E-107	AB032283.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1563	6712	11903	3.56	1.0E-107	BF087405.1	EST_HUMAN	OV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
1764	6880	12096	2.27	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin 2 precursor (CTSZ) gene, exon 3
1853	6974	12195	2.84	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1853	6974	12196	2.84	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2342	7449	12703	2.18	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2342	7449	12704	2.18	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2506	7609	12860	1.51	1.0E-107	BE732480.1	EST_HUMAN	601567619F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3842309 5'
2506	7609	12861	1.51	1.0E-107	BE732480.1	EST_HUMAN	601567619F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3842309 5'
2879	8133	13295	4.68	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2879	8133	13296	4.68	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3074	8227	13378	3.46	1.0E-107	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
3806	8942	14050	4.44	1.0E-107	AF020871.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
950	6104	11273	2.51	1.0E-108	BE298042.1	EST_HUMAN	601177019F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3592348 5'
1269	6398	11571	6.07	1.0E-108	Y18000.1	NT	Homo sapiens NF2 gene
2070	7186	12427	2.92	1.0E-108	BF026728.1	EST_HUMAN	601871914F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3954939 5'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2311	7420	12670	1.13	1.0E-108	AI686040.1	EST_HUMAN	t891e10.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
2311	7420	12671	1.13	1.0E-108	AI686040.1	EST_HUMAN	t891e10.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
2405	7511	12761	65.48	1.0E-108	BE206894.1	EST_HUMAN	bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863899 3' similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
2928	8083	13250	1.27	1.0E-108	6005978	NT	Homo sapiens Kruppel-like factor 8 (KLIF), mRNA
3331	8477	13640	0.63	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3331	8477	13641	0.63	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4129	9257	14395	1.35	1.0E-108	AW564438.1	EST_HUMAN	t112a11.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE P56104 SH3-BINDING PROTEIN 3BP-1;
4500	9619	14760	5.12	1.0E-108	U72951.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4772	9885	15031	2.17	1.0E-108	U72951.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4897	10008	15153	1.09	1.0E-108	AW504759.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4927	10037	15177	2.75	1.0E-108	AJ008005.1	NT	Homo sapiens PSN1 gene, alternative transcript
5116	10217	15352	0.67	1.0E-108	5031824	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
5141	10241	15377	1.15	1.0E-108	Y12490.1	NT	Homo sapiens nebulin (NEB), mRNA
5149	10249	15388	1.49	1.0E-108	8400716	NT	Homo sapiens nebulin (NEB), mRNA
5204	10301		3.35	1.0E-108	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
41	5252	10370	2.06	1.0E-109	AW803116.1	EST_HUMAN	IL2-UM0077-260400-079-D06 UM0077 Homo sapiens cDNA
64	5274	10409	3.56	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
216	5410	10550	0.72	1.0E-109	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
225	5418	10555	4.54	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
466	5634	10772	4.05	1.0E-109	4507712	NT	Homo sapiens tetrapeptide repeat domain 2 (TTC2) mRNA
598	5758	10886	26.83	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
598	5758	10887	26.83	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1013	6166	11322	0.61	1.0E-109	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1205	6336	11508	37.97	1.0E-109	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
1209	6338	11508	20.28	1.0E-109	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
1556	6685	11872	2.97	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
1556	6685	11873	2.97	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
1884	7004	12223	9.05	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0016 protein, partial cds

Page 165 of 214  
Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2223	7335	12589	1.78	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2231	7343	12597	3.7	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2587	7688	12943	4.89	1.0E-109	AI022326.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 O02197 CIRCULATING CATHODIC ANTIGEN.;
2587	7688	12944	4.89	1.0E-109	AI022326.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 O02197 CIRCULATING CATHODIC ANTIGEN.;
2588	7689	12945	1.95	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCY1A) mRNA
3030	8184	13339	2.43	1.0E-109	N85190.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3369	8514	13681	1.01	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA
3369	8514	13682	1.01	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA
3503	8644	13810	1.13	1.0E-109	AF240598.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3545	8686	13848	0.99	1.0E-109	M37928.1	NT	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
3545	8686	13849	0.99	1.0E-109	M37928.1	NT	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
3819	8956		1.28	1.0E-109	BE146144.1	EST_HUMAN	MR0-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA
3988	9103	14251	0.97	1.0E-109	AB011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
3988	9103	14252	0.97	1.0E-109	AB011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
4118	9246	14383	3.75	1.0E-109	AI655417.1	EST_HUMAN	ts98e06.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP.F53A2.8 CE16100;
4383	9504	14647	2.77	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCY1A) mRNA
4573	9691	14828	1.56	1.0E-109	7662083	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
4904	10014	15158	0.99	1.0E-109	R15400.1	EST_HUMAN	ye48e06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53057 5'
5034	10136	15288	0.63	1.0E-109	BE293873.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
5034	10136	15269	0.63	1.0E-109	BE293873.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
3	5216	10327	0.75	1.0E-110	7549804	NT	Homo sapiens diiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
36	5247	10364	3.66	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
36	5247	10365	3.66	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
105	5215	10327	0.86	1.0E-110	7549804	NT	Homo sapiens diiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
292	5480	10622	0.76	1.0E-110	D87291.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
525	5691	10823	1.39	1.0E-110	U84550.1	NT	Human dystrobrevin (DTN) gene, exon 20
1182	6317	11485	1.01	1.0E-110	5031620	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1283	6412	11598	2.49	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1926	7045	12266	1.67	1.0E-110	BE379477.1	EST_HUMAN	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3009883 5'
2050	7166		0.98	1.0E-110	BF508886.1	EST_HUMAN	UHH-BI4-aos-b-05-0-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'

Page 166 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2803	7989		0.88	1.0E-110	4503098	NT	Homo sapiens chondralin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3002	6412	11588	1.48	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
3059	8212		1.12	1.0E-110	U76027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
4179	9301	14437	2.25	1.0E-110	M15918.1	NT	Human autoimmune antigen small nuclear ribonucleoprotein E, pseudogene
4603	9721	14855	2.31	1.0E-110	A1017213.1	EST_HUMAN	alpha32b10.x1 Soares_NFL_T_C8C_31 Homo sapiens cDNA clone IMAGE:1627963 3' similar to
4823	9741	14883	4.09	1.0E-110	AU117812.1	EST_HUMAN	SW:M121_RAT_P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4958	10066		2.28	1.0E-110	7682441	NT	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
6165	10263	15402	7.72	1.0E-110	A1791362.1	EST_HUMAN	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
170	5365		42.79	1.0E-111	U43701.1	NT	ch64402.y6 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1471779 5'
193	5368	10531	0.61	1.0E-111	4758807	NT	Human ribosomal protein L23a mRNA, complete cds
733	5889		2.03	1.0E-111	BF035327.1	EST_HUMAN	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
742	5898	11051	3.32	1.0E-111	8393002	NT	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
928	6076	11245	2.2	1.0E-111	M25142.1	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
3877	8816	13972	1.05	1.0E-111	6912841	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
3877	8816	13973	1.05	1.0E-111	6912641	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
4142	9270	14408	1.08	1.0E-111	7681569	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
4306	9428	14563	4.63	1.0E-111	K02268.1	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
605	5765	10893	0.78	1.0E-112	4601854	NT	Human enkephalin B (enkeB) gene, exon 4 and 3' flank and complete cds
607	5767	10895	4.13	1.0E-112	U29103.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
607	5767	10896	4.13	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
631	5791	10924	1.98	1.0E-112	BF508036.1	EST_HUMAN	U1-H-B14-aot-g-04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2400811 3'
631	5791	10925	1.98	1.0E-112	BF508036.1	EST_HUMAN	U1-H-B14-aot-g-04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1002	6148	11315	1.22	1.0E-112	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1063	6204	11366	2.27	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1698	6826	12025	4.1	1.0E-112	7682126	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1698	6826	12026	4.1	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2181	7284	12541	0.98	1.0E-112	A1766925.1	EST_HUMAN	W90006.x1 NCI_CGAP_Ket12 Homo sapiens cDNA clone IMAGE:2400811 3'
2478	7593	12833	1.67	1.0E-112	BE866856.1	EST_HUMAN	601442874F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3876958 5'
3050	8204		0.76	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3961	8997	14154	0.66	1.0E-112	BE076073.1	EST_HUMAN	MR2-BT0590-090300-113-f09 BT0590 Homo sapiens cDNA
4577	9095	14832	0.9	1.0E-112	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4717	9832	14975	5.79	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds

Page 187 of 214  
Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4717	9832	14976	5.79	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
741	5897	11049	7.68	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
741	5897	11050	7.68	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
942	6090	11268	39.98	1.0E-113	M11965.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1555	6884	11871	3.46	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
1943	7873	12285	1.77	1.0E-113	AF240775.1	NT	Homo sapiens eIF4E-transporter mRNA, complete cds
2086	7202	12446	1.23	1.0E-113	BF515218.1	EST_HUMAN	U1H-BW1-ant-f-03-D-U1.s1 NCJ_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
2431	7535	12788	4.66	1.0E-113	AJ008976.1	NT	Homo sapiens PLP gene
3107	8260	13414	3.16	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5049	10151	15281	0.6	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5049	10151	15282	0.6	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
57	5268	10397	3.85	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
57	5268	10398	3.85	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
57	5268	10399	3.85	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
644	5805	10940	5.72	1.0E-114	T70551.1	EST_HUMAN	yd15c01.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element;
1072	6212	11376	4.74	1.0E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1317	6446	11625	7.17	1.0E-114	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1654	6782	11975	3.61	1.0E-114	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
1686	6815	12013	10.86	1.0E-114	8878073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2074	7190	12433	3.62	1.0E-114	BE171984.1	EST_HUMAN	MRO-HT0459-250200-002-d07 HT0359 Homo sapiens cDNA
2236	7348	12803	1.19	1.0E-114	AB002374.1	NT	Human mRNA for KIAA0376 gene, partial cds
2765	5254	10373	1.13	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2765	5254	10374	1.13	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3108	8261	13415	2.8	1.0E-114	X04086.1	NT	Human gene for catenase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3151	8302	13462	1.01	1.0E-114	BF206374.1	EST_HUMAN	G01869932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
3991	9125	14270	1.35	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4192	9318	14451	1	1.0E-114	AA574056.1	EST_HUMAN	nk11d02.s1 NCJ_CGAP_Co2 Homo sapiens cDNA clone IMAGE:1013187 3' similar to gb:X65857_cds1
4369	9490	14634	0.78	1.0E-114	J03171.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
5118	10219	15353	1.43	1.0E-114	BE275324.1	EST_HUMAN	Human interferon-alpha receptor (HuIFN-alpha-Rce) mRNA, complete cds
22	5233	10347	10.03	1.0E-115	4758111	NT	G01122173F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346099 5'
125	5323	10463	4.96	1.0E-115	4505936	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
							Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220KD) (POLR2A) mRNA

Page 168 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
129	5327		52.4	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
290	5478	10619	9.75	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-508 UM0094 Homo sapiens cDNA
534	5700	10832	1.52	1.0E-115	AI399206.1	EST_HUMAN	q06f01.xt NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-I INTERACTING PEPTIDE 5;
534	5700	10833	1.52	1.0E-115	AI399206.1	EST_HUMAN	q06f01.xt NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-I INTERACTING PEPTIDE 5;
787	5941	11100	1.26	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
787	5941	11101	1.26	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
789	5943	11103	196.09	1.0E-115	4503794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1574	6702	11890	1.49	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1574	6702	11891	1.49	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1840	6961	12184	1.89	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
2072	7188	12429	1.22	1.0E-115	BE745469.1	EST_HUMAN	Homo sapiens partial TTN gene for titin
2072	7188	12430	1.22	1.0E-115	BE745469.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2275	7395	12634	1.35	1.0E-115	AF231124.1	NT	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2813	7669		1.84	1.0E-115	AW804759.1	EST_HUMAN	Homo sapiens testican-1 mRNA, complete cds
3091	8244	13394	3.74	1.0E-115	AJ245922.1	NT	QV4-UM0094-300300-156-508 UM0094 Homo sapiens cDNA
3091	8244	13395	3.74	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3454	8596	13760	2.04	1.0E-115	AJ277892.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
4016	9149	14291	4.51	1.0E-115	AB002348.2	NT	Homo sapiens partial TTN gene for titin
4240	9365	14498	0.73	1.0E-115	AL137163.1	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4380	9501	14644	3.37	1.0E-115	6912659	NT	Novel human gene mapping to chromosome X
4413	9533	14672	3.17	1.0E-115	4789279	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4647	9765	14809	3.36	1.0E-115	AL098857.1	NT	Homo sapiens EphA4 (EPHA4) mRNA
4647	9765	14910	3.36	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4879	9890	15136	2.95	1.0E-115	AL193288.2	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4879	9890	15137	2.95	1.0E-115	AL193288.2	NT	Homo sapiens chromosome 21 segment HS21C088
571	5735	10863	1.37	1.0E-116	BE275502.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C068
801	5955	11115	1.24	1.0E-116	4507334	NT	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988875 5'
860	6011		0.63	1.0E-116	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1998	7115	12350	1.69	1.0E-116	5174478	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1998	7115	12351	1.69	1.0E-116	5174478	NT	Homo sapiens pericentriin (PCNT) mRNA
2018	7136	12376	2.34	1.0E-116	AU133080.1	EST_HUMAN	Homo sapiens pericentriin (PCNT) mRNA
2088	7632	12447	1.18	1.0E-116	MT19824.1	NT	AU133080 NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5'
							Human apolipoprotein B-100 (apoB) gene, exons 17 and 18

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2088	7932	12448	1.18	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2284	7393	12644	1.09	1.0E-116	5453941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2322	7430		1.27	1.0E-116	U78308.1	NT	Human olfactory receptor pseudo cfr17-01 (OR17-01) pseudogene, complete cds
2433	7537	12790	2.13	1.0E-116	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2686	7880	13043	4.58	1.0E-116	BE889256.1	EST_HUMAN	601513337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'
3154	8305	13464	5.46	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3154	8305	13465	5.46	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4357	9479	14617	2.21	1.0E-116	5031954	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4453	9572	14711	1.62	1.0E-116	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4826	9937	15078	1.66	1.0E-116	AB07096.1	EST_HUMAN	PM-BT135-070499-016 BT135 Homo sapiens cDNA
5033	10135	15266	1.18	1.0E-116	U59109.1	NT	Mus musculus nebulin mRNA, partial cds
5033	10135	15267	1.18	1.0E-116	U59109.1	NT	Mus musculus nebulin mRNA, partial cds
557	5722	10853	9.66	1.0E-117	4826636	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1078	7908	11384	2.2	1.0E-117	AF124393.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
1228	6360	11530	1.2	1.0E-117	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1845	6966	12187	1.38	1.0E-117	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
2193	7305	12555	3.45	1.0E-117	AW957699.1	EST_HUMAN	EST369769 MAGE resequences, MAGE Homo sapiens cDNA
3251	8401	13563	1.68	1.0E-117	AA978114.1	EST_HUMAN	op32c11.s1 Soares NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'
3965	9100	14249	5.62	1.0E-117	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4321	9443	14576	1.76	1.0E-117	8656564	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4550	9668	14810	3.06	1.0E-117	AL042120.1	EST_HUMAN	DKFZp434C1120_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1120 5'
4692	9808	14954	1.08	1.0E-117	X89670.1	NT	H. sapiens mRNA for TPCR16 protein
4692	9808	14955	1.08	1.0E-117	X89670.1	NT	H. sapiens mRNA for TPCR16 protein
4778	9891	15037	10.26	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4778	9891	15038	10.26	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4839	9951	15095	1.5	1.0E-117	U58109.1	NT	Mus musculus nebulin mRNA, partial cds
4839	9951	15096	1.5	1.0E-117	U58109.1	NT	Mus musculus nebulin mRNA, partial cds
4917	10027	15169	3.3	1.0E-117	AB020573.1	NT	Homo sapiens mRNA for KIAA0806 protein, complete cds
69	5279	10415	7.76	1.0E-118	AF161500.1	NT	Homo sapiens HSPC151 mRNA, complete cds
91	5300	10439	1.53	1.0E-118	AL045854.1	EST_HUMAN	DKFZp434I056_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434I056 5'
515	5681	10815	11.4	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (D328E19.C1.1), mRNA

Page 170 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
915	7904	11231	2.6	1.0E-118	5174880	NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2214	7326	12576	3.87	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2214	7326	12577	3.87	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2214	7326	12578	3.87	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2310	7419		19.78	1.0E-118	AW951729.1	EST_HUMAN	EST363789 MAGE resequences. MAGB Homo sapiens cDNA
2703	7799	13050	6.32	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2703	7799	13051	6.32	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3080	8233		4.24	1.0E-118	Y13932.1	NT	Homo sapiens PRKY exon 7
3178	8329	13492	4.93	1.0E-118	A1347694.1	EST_HUMAN	qp01f05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1918769 3'
3178	8329	13493	4.93	1.0E-118	A1347694.1	EST_HUMAN	qp01f05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1918769 3'
3921	9057	14216	0.99	1.0E-118	AB024469.1	NT	Pongo pygmaeus DNA, similar to pol gene of HERV-W and MSRV, isolate: ORW3-3
4055	9195	14334	8.96	1.0E-118	D23680.1	NT	Human mRNA for ribosomal protein, complete cds
4675	9791	14937	1.17	1.0E-119	11426793	NT	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA
756	5911	11089	0.63	1.0E-119	AF170492.1	NT	Homo sapiens chloride channel CLCA (CLCA) mRNA, complete cds
1039	7907	11344	1.69	1.0E-119	7705607	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
1937	7056	12277	3.67	1.0E-119	AB023147.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3077	8230	13382	0.94	1.0E-119	8922205	NT	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
3926	9061	14219	1.07	1.0E-119	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
299	5487	10628	0.77	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1043	6184	11350	2.38	1.0E-120	AF246540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1043	6184	11351	2.38	1.0E-120	AF246540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1434	6561	11744	5.03	1.0E-120	N44873.1	EST_HUMAN	yy40g12.r1 Soares melanocyte 2/NbHM Homo sapiens cDNA clone IMAGE:273766 5'
1615	6743	11938	2.55	1.0E-120	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1818	6941	12159	4.32	1.0E-120	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2098	7213	12460	2.02	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2098	7213	12461	2.02	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2500	7604	12852	1.23	1.0E-120	4755124	NT	Homo sapiens aquaporin 4 (AQP4), splice variant b, mRNA
3289	5487	10628	1.13	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4335	9457	14594	1.71	1.0E-120	AF066490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4335	9457	14595	1.71	1.0E-120	AF066490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4632	9790	14890	1.79	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4632	9790	14897	1.79	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
72	5281	10419	0.87	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
376	5554	10698	2.09	1.0E-121	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'



Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
722	7898	11026	1.11	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1597	8718	11908	0.99	1.0E-121	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
1969	7086	12312	1.31	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
1969	7086	12313	1.31	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2093	7208	12454	1.15	1.0E-121	L76631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2540	7643	12892	1.37	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150286 5'
2540	7643	12893	1.37	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150286 5'
2938	8092	13289	1.11	1.0E-121	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
3053	8206	13361	5.9	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3053	8206	13362	5.9	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3524	8665	13832	1	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3524	8665	13833	1	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3655	8794	13950	7.87	1.0E-121	AF155166.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
3704	8842	13997	0.7	1.0E-121	AI904151.1	EST_HUMAN	GM-BT043-090299-075 BT043 Homo sapiens cDNA
4307	9429	14564	1.48	1.0E-121	AI263294.1	EST_HUMAN	qx57601.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3'
4961	10069	15205	2.74	1.0E-121	X91937.1	NT	H. sapiens ECE-1 gene (exon 17)
265	5455	10593	1.78	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
334	5517	10653	2.2	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
365	5636	10677	1.98	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
863	6033	11205	3.01	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
1222	6354	11524	5.81	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1727	6854	12059	2.28	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1727	6854	12060	2.28	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1826	6949	12171	3.48	1.0E-122	BE906024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899358 5'
2464	7568	12621	22.83	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2464	7568	12622	22.83	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2801	7958	13122	2.09	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FVE-DSP2 mRNA, complete cds
4815	9927	15068	2.79	1.0E-122	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (precursor nexin-II, Alzheimer disease) (APP), mRNA
4975	10083		1.34	1.0E-122	AW504645.1	EST_HUMAN	U1-HF-BND-ali-a-03-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076948 5'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
185	5380	10521	0.84	1.0E-123	U31519.1	NT	Human phosphoenolpyruvate carboxylase (PCK1) gene, promoter region and partial cds
768	5922	11078	2.61	1.0E-123	BF345274.1	EST_HUMAN	602018059F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4153670 5'
768	5922	11080	2.61	1.0E-123	BF345274.1	EST_HUMAN	602018059F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4153670 5'
1014	6157	11323	4.85	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1023	6164	11330	5.61	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (INMT), mRNA
1242	6372	11547	11.95	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1242	6372	11548	11.95	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
2090	7205	12450	2.04	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2090	7205	12451	2.04	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2090	7205	12452	2.04	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2293	7402		1.6	1.0E-123	7705962	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
266	5456	10594	1.6	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
266	5456	10595	1.6	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
272	5462		1.57	1.0E-124	D87876.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
485	5653	10792	2.1	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
689	5845	10988	3.14	1.0E-124	AA397551.1	EST_HUMAN	z181b04.r1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
689	5846	10989	3.14	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
757	5912	11070	6.92	1.0E-124	AF155654.1	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
809	5962	11124	1.58	1.0E-124	4507500	NT	Human putative ribosomal protein S1 mRNA
905	6055	11224	3.62	1.0E-124	7705448	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1319	6448	11628	0.74	1.0E-124	11419092	NT	Homo sapiens hypothetical protein (HSPC068), mRNA
1353	6482	11661	4.17	1.0E-124	AF274892.1	NT	Homo sapiens ring finger protein (RNF), mRNA
1353	6482	11662	4.17	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1827	6950	12172	3.71	1.0E-124	AJ131712.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2054	7170	12409	1.39	1.0E-124	BE878624.1	EST_HUMAN	Homo sapiens mRNA for nuclear RNA-helicase (ncl-h61 gene)
2434	7538	12791	1.68	1.0E-124	AB024009.1	NT	601491716F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893954 5'
3471	8913	13779	0.84	1.0E-124	S78684.1	NT	Homo sapiens gene for B120, exon 11
3471	8913	13780	0.84	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3876	9012	14169	0.8	1.0E-124	4507500	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
4051	9182	14324	0.73	1.0E-124	4504116	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
							Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA

Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4710	9826	14969	1.71	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
317	5503		1.1	1.0E-125	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
425	5212	10324	3.84	1.0E-125	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5'
643	5804	10938	0.64	1.0E-125	A11106556.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
643	5804	10939	0.64	1.0E-125	A11106556.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
726	5882	11030	1.81	1.0E-125	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
861	6012	11183	3.17	1.0E-125	AA042813.1	EST_HUMAN	z53c07.s1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65957_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
999	6145	11312	1.51	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1155	6281	11454	1.2	1.0E-125	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1823	6946	12167	3.61	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1823	6946	12168	3.61	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
2338	7445	12697	2.98	1.0E-125	AA011278.1	EST_HUMAN	z01g09.r1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:423568 5'
2474	7578	12830	2.38	1.0E-125	AA042813.1	EST_HUMAN	z53c07.s1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65957_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2559	7661	12814	1.66	1.0E-125	4504698	NT	Homo sapiens inhibin, alpha (INH) mRNA
2559	7661	12915	1.66	1.0E-125	4504698	NT	Homo sapiens inhibin, alpha (INH) mRNA
2563	7664	12919	11.32	1.0E-125	A1732966.1	EST_HUMAN	gb74f08.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048131 5' similar to TR:O95604 O95604 ZINC FINGER PROTEIN;
2881	10303	13299	1	1.0E-125	BE018009.1	EST_HUMAN	z53c07.s1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65957_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
3837	8973	14129	1.42	1.0E-125	AA042813.1	EST_HUMAN	z53c07.s1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65957_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
4523	9641	14786	1.94	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4523	9641	14789	1.94	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4588	9706	14844	1.96	1.0E-125	BE315412.1	EST_HUMAN	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140786 5'
774	5928	11087	2.04	1.0E-126	4758007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
777	5931	11090	1.04	1.0E-126	M61936.1	NT	Human laminin B1 chain gene, exon 20
919	6068	11233	0.97	1.0E-126	X68795.1	NT	H. sapiens gene for alphas1-antichymotrypsin, exon 3
2325	7433	12685	1.42	1.0E-126	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2325	7433	12686	1.42	1.0E-126	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2560	7662	12916	3.07	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3044	8198	13354	7.24	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stratagene pancreas (#637208) Homo sapiens cDNA clone IMAGE:592420 5'
3044	8198	13355	7.24	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stratagene pancreas (#637208) Homo sapiens cDNA clone IMAGE:592420 5'
3609	8748	13904	1.24	1.0E-126	X53941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene

Page 174 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3632	8771	13927	2.35	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4802	9915	15056	1.67	1.0E-126	N34078.1	EST_HUMAN	W7806.1 Scores melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:267850 5'
167	5363	10504	8.45	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
167	5363	10505	8.45	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
168	5363	10504	7	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
168	5363	10505	7	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
271	5461	10602	1.52	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
271	5461	10603	1.52	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
882	6032	11204	1.34	1.0E-127	AF114488.1	NT	Homo sapiens interseclin short isoform (ITSN) mRNA, complete cds
1705	6833	12034	1.99	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2058	7174	12412	1.78	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2058	7174	12413	1.78	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2184	7297	12545	47.43	1.0E-127	4508620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2323	7431	12683	3.12	1.0E-127	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
2573	7673	12928	49.35	1.0E-127	X12881.1	NT	Human mRNA for cytochrome 18
2585	7686	12940	1	1.0E-127	AA450131.1	EST_HUMAN	z42a02.1 Scores, total, fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'
2585	7686	12941	1	1.0E-127	AA450131.1	EST_HUMAN	z42a02.1 Scores, total, fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'
3788	8925	14075	1	1.0E-127	AW161297.1	EST_HUMAN	eu80e06.y1 Schnelder fetal brain 00004 Homo sapiens cDNA clone IMAGE:2792594 5' similar to TR:Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ; contains element MER22 repetitive element ;
4230	9355	14487	19.81	1.0E-127	7708239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4230	9355	14488	19.81	1.0E-127	7708239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4473	9592	14731	0.73	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 rethroid metabolizing protein P450RAI-2 mRNA, complete cds
4576	9694	14831	4.77	1.0E-127	4508384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4601	9719		2.3	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C058
4644	9782	14907	1.49	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
459	5627	10767	2.94	1.0E-128	BE385617.1	EST_HUMAN	G01276127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'
2063	7179	12417	80.69	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2063	7179	12418	80.69	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2191	7303	12553	172.11	1.0E-128	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2422	7527		6.08	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3375	8520	13684	1.11	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4634	9752	14899	5.88	1.0E-128	11426673	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
117	6680	10730	3.07	1.0E-129	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
412	5580	10730	3.48	1.0E-129	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1733	6660	12063	5.33	1.0E-129	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1737	6864	12067	1.65	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1737	6864	12068	1.66	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1857	6977	12199	3.1	1.0E-129	11418622	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
3105	8258	13409	1.84	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3105	8258	13410	1.84	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3105	8258	13411	1.84	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4135	9263	14402	2.01	1.0E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
							CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
4264	9379	14510	2.21	1.0E-129	AW755254.1	EST_HUMAN	Cardiomyopathy associated gene 5
							CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
4254	9379	14511	2.21	1.0E-129	AW755254.1	EST_HUMAN	Cardiomyopathy associated gene 5
75	5284	10423	2.24	1.0E-130	7705530	NT	Homo sapiens hypothetical protein (HSPC242), mRNA
1172	6307	11474	0.97	1.0E-130	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1680	6809	12007	36.02	1.0E-130	BE275192.1	EST_HUMAN	601121935F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3348366 5'
1680	6809	12008	36.02	1.0E-130	BE275192.1	EST_HUMAN	601121935F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3348366 5'
1885	7102		2.3	1.0E-130	X04092.1	NT	Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2733	7827		3.54	1.0E-130	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2844	7989	13157	1.28	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
2844	7989	13158	1.29	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3563	8706	13867	0.8	1.0E-130	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3748	7999	13157	5.46	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3748	7999	13158	5.46	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3909	9045	14204	1.33	1.0E-130	AW503580.1	EST_HUMAN	UI-HF-BND-aky-g-06-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4048	9179	14320	1.05	1.0E-130	M97710.1	NT	Human T-cell receptor (V alpha 22.1, J alpha 1) mRNA
4511	9530	14774	6.92	1.0E-130	AW843993.1	EST_HUMAN	CM4-CN0045-180200-511-102 CN0045 Homo sapiens cDNA
5082	10183	15320	1.33	1.0E-130	AW363298.1	EST_HUMAN	RCO-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
5082	10183	15321	1.33	1.0E-130	AW363298.1	EST_HUMAN	RCO-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4	5216	10328	1.91	0.0E+00	AA228126.1	EST_HUMAN	z68c04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:687590 5' similar to TR:G222811
4	5216	10329	1.91	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
7	5216	10332	3.34	0.0E+00	4885136	NT	z68c04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:687590 5' similar to TR:G222811
14	5225	10337	1.38	0.0E+00	8923349	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
14	5225	10338	1.38	0.0E+00	8923349	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
21	5232	10345	13.75	0.0E+00	D83327.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
21	5232	10346	13.75	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
26	5236	10360	51.42	0.0E+00	AF141349.1	NT	Homo sapiens DORR1 mRNA, partial cds
33	5244	10360	1.99	0.0E+00	5802697	NT	Homo sapiens beta-tubulin mRNA, complete cds
35	5246	10303	0.77	0.0E+00	M59600.1	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
39	5250	10368	9.5	0.0E+00	6857825	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
56	5267	10395	12.92	0.0E+00	Y17151.2	NT	Homo sapiens FNA-binding protein S1, serine-rich domain (RNPS1), mRNA
58	5267	10396	12.92	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
58	5269	10400	6.86	0.0E+00	D78804.1	EST_HUMAN	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
58	5269	10401	6.86	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-516H08 5'
59	5270	10402	37.3	0.0E+00	L16558.1	NT	HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-516H08 5'
61	5272	10405	13.22	0.0E+00	AW069534.1	EST_HUMAN	Human ribosomal protein L7 (RPL7) mRNA, complete cds
61	5272	10406	13.22	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMISC_cr48e07 3'
65	5275	10410	1.1	0.0E+00	M60676.1	NT	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMISC_cr48e07 3'
66	5276		0.79	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
74	5283	10421	1.92	0.0E+00	4758977	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
74	5283	10422	1.92	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
78	5287	10427	0.72	0.0E+00	4501850	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
78	5288		31.31	0.0E+00	4504444	NT	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
87	5296	10435	84.52	0.0E+00	5016088	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
90	5299	10438	71.3	0.0E+00	U99277.1	NT	Homo sapiens actin, beta (ACTB) mRNA
97	5306	10445	4.27	0.0E+00	A114743.1	EST_HUMAN	Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds
98	5307	10446	1.52	0.0E+00	AB037784.1	NT	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
112	5316	10455	1.5	0.0E+00	A1823701.1	EST_HUMAN	Homo sapiens mRNA for KIAA1363 protein, partial cds
							ts38b05.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:230833 3' similar to TR:Q99551
							MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR ;

Page 177 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
113	5316	10455	3.14	0.0E+00	AI623701.1	EST_HUMAN	ts38605.x1 NCJ_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551
114	7860	10456	4.81	0.0E+00	N36040.1	EST_HUMAN	MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR ;
114	7860	10457	4.81	0.0E+00	N36040.1	EST_HUMAN	Yw01h09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5'
126	5324	10469	5.01	0.0E+00	4505938	NT	Yw01h09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5'
128	5324	10470	5.01	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
134	5568	10714	1.62	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
136	5332	10477	1.43	0.0E+00	T56945.1	EST_HUMAN	Yab3g04.r2 Stralagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
136	5332	10478	1.43	0.0E+00	T56945.1	EST_HUMAN	Yab3g04.r2 Stralagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
148	5345	10495	24.18	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
152	5349	10491	6.08	0.0E+00	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3883803 5'
154	5351	10492	83.55	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
157	5354	10494	0.85	0.0E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
159	5356	10495	4.11	0.0E+00	BE285973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528864 5'
160	5356	10495	3.81	0.0E+00	BE285973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528864 5'
161	5357	10496	7.12	0.0E+00	W73973.1	EST_HUMAN	Zd62605.r1 Soares_fetal_heart_NBRH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to
162	5358	10497	2.97	0.0E+00	BE162832.1	EST_HUMAN	gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
162	5358	10498	2.87	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-404 HT0457 Homo sapiens cDNA
163	5359	10499	3.87	0.0E+00	AF244088.1	NT	QV3-HT0457-140200-088-404 HT0457 Homo sapiens cDNA
166	5362	10502	57.01	0.0E+00	AL163202.2	NT	Homo sapiens zinc finger protein mRNA, complete cds
166	5362	10503	57.01	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
176	5370	10510	6.34	0.0E+00	BE018970.1	EST_HUMAN	b524e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
176	5370	10511	6.34	0.0E+00	BE018970.1	EST_HUMAN	CE22631 ;
181	5375	10514	7.66	0.0E+00	AB018327.1	NT	b524e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
181	5375	10515	7.66	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
182	5376	10516	6.19	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
182	5376	10517	6.19	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	5386	10526	309.91	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
196	5391	10534	13.52	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
196	5391	10535	13.52	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
198	5393	10537	7.31	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds

Page 178 of 214  
Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
198	5353	10538	7.31	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
207	7885	10544	27.02	0.0E+00	AF587308.1	EST_HUMAN	U0408.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);
207	7885	10545	27.02	0.0E+00	AF587308.1	EST_HUMAN	U0408.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);
209	5403	10547	2.59	0.0E+00	AF156658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
212	5406		53.6	0.0E+00	4506632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
213	5407		8.58	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
219	5413	10552	4.01	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
220	5413	10552	2.98	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
221	5414	10553	4.61	0.0E+00	6878444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspyl), mRNA
235	5428	10568	22.84	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
237	5430		14.18	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21 C001
244	5435	10574	3.02	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
246	5437	10577	1.02	0.0E+00	X89772.1	NT	H. sapiens mRNA for Interferon alpha/beta receptor (long form)
254	5445		6.18	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
267	5457	10596	1.45	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
267	5457	10597	1.45	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
269	5459	10599	2.13	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
280	5469		4.7	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
281	5470	10612	5.27	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
281	5470	10613	5.27	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
282	5471		1.16	0.0E+00	AW845283.1	EST_HUMAN	IL2-CT0031-T81198-020-803 CT0031 Homo sapiens cDNA
291	5479	10620	5.27	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
291	5479	10621	5.27	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
302	5480	10631	14.01	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
303	5491	10632	7.12	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
304	7888		24.79	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
305	5482	10633	0.93	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART) mRNA
306	5493		3.88	0.0E+00	AA480002.1	EST_HUMAN	z18c06.r1 Soares_NHMFu_S1 Homo sapiens cDNA clone IMAGE:753994 5'
307	5494	10634	17.26	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
308	5494	10634	18.94	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
312	5498	10638	2.05	0.0E+00	AF114488.1	NT	Homo sapiens interseectin short isoform (ITSN) mRNA, complete cds



Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
325	5510	10647	1.9	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
325	5510	10648	1.9	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
326	5511	10649	3.19	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
327	5511	10649	2.21	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
342	5525	10661	5.87	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
345	5528	10665	43.24	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
348	5531	10670	2.56	0.0E+00	U71600.1	NT	Human zinc finger protein zfp31 (zfp31) mRNA, partial cds
353	5535	10674	2.88	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
353	5535	10675	2.88	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
354	7889	10676	2.95	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
356	5537	10678	1.14	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
359	5540	10682	1.84	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
360	5541	10683	2.71	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
361	5541	10683	2.65	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
363	5543	10685	1.05	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
374	5552	10696	4.43	0.0E+00	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
385	5594	10740	7.75	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
386	5595	10741	2.53	0.0E+00	AJ363014.1	EST_HUMAN	qy81h05.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54189
391	5560	10703	4.73	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (HUMAN);
394	5562	10706	2.69	0.0E+00	4503880	NT	RC2-C10320-300100-016-a09 CT0320 Homo sapiens cDNA
395	5563	10707	2.17	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
396	5563	10708	2.17	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
396	5564	10709	1.86	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
397	5565	10710	2.01	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
397	5565	10711	2.01	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
398	5566	10712	2.45	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
399	5567	10713	3.28	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
400	5568	10714	2.6	0.0E+00	4503880	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
401	5569	10715	3.22	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
401	5569	10716	3.22	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
402	5569	10715	3.76	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
402	5569	10716	3.76	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
406	5573		752.9	0.0E+00	4506808	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
419	5206	10318	1.15	0.0E+00	R17795.1	EST_HUMAN	yg09a02.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31652 5'
427	5596	10742	1.21	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
428	5597		20.02	0.0E+00	4508723	NT	phosphoribosylaminimidazole synthetase (GART) mRNA
429	5598	10743	6.43	0.0E+00	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
430	5599	10744	15.73	0.0E+00	4507152	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
430	5599	10745	15.73	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
431	5600	10746	6.04	0.0E+00	AF193607.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
443	5611		1.6	0.0E+00	AL163201.2	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
445	5613	10759	1.95	0.0E+00	4557879	NT	Homo sapiens chromosome 21 segment HS21C001
450	5618		1.13	0.0E+00	AA324262.1	EST_HUMAN	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
461	5619		1.64	0.0E+00	BE264447.1	EST_HUMAN	EST27054 Cerebellum II Homo sapiens cDNA 5' end
467	5635	10773	3.39	0.0E+00	4504532	NT	601111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
467	5635	10774	3.39	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
473	5640	10782	55.72	0.0E+00	4557887	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
473	5640	10783	55.72	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
483	5651	10789	4.42	0.0E+00	AL163246.2	NT	Homo sapiens keratin 18 (KRT18) mRNA
484	5652	10790	5.18	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
484	5652	10791	5.18	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
493	5660	10790	3.46	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
495	5662	10798	1.68	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
503	5670	10804	3.16	0.0E+00	BE385144.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
504	7802	10805	1.26	0.0E+00	AW098825.1	EST_HUMAN	PM0-DJ10065-130400-002-c06 DT0065 Homo sapiens cDNA
507	5673	10807	2.7	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
508	5674	10808	1.29	0.0E+00	8923655	NT	Homo sapiens PC329 protein (PC329), mRNA
517	5683	10817	5.2	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
524	7893	10821	1.96	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
529	5695	10827	1.37	0.0E+00	BF028005.1	EST_HUMAN	601764858F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996908 5'
535	5701	10834	2.3	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
538	5704	10837	19.21	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
539	5705	10838	4.52	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
539	5705	10839	4.52	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
541	5707	10841	5.08	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
542	5708	10842	2.92	0.0E+00	8923831	NT	Homo sapiens anillin (LOC544443), mRNA
542	5708	10843	2.92	0.0E+00	8923831	NT	Homo sapiens anillin (LOC544443), mRNA
547	5712		5.28	0.0E+00	AF003528.1	NT	Homo sapiens X-linked ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
555	5720	10852	2.09	0.0E+00	AW135324.1	EST_HUMAN	U1-H-B1-ach-h-04-D-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
565	5730		4.68	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
584	5747	10876	4.19	0.0E+00	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA
587	5759		3.99	0.0E+00	J04066.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
600	5762	10890	2.17	0.0E+00	BF104898.1	EST_HUMAN	601822627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
606	5766	10894	0.57	0.0E+00	4501854	NT	Homo sapiens acyl-Coenzyme A carboxylase beta (ACACB), mRNA
611	5771	10900	1	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
611	5771	10901	1	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
621	5781	10911	2.78	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
623	5783	10914	2.3	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1396 protein, partial cds
625	5785	10916	1.54	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
626	5786	10918	1.9	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
626	5786	10917	1.9	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
627	5787	10918	0.89	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
627	5787	10919	0.89	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
634	5795	10929	1.16	0.0E+00	AA399486.1	EST_HUMAN	z60c07.r1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:726732 5'
638	5799	10933	5.06	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
642	5803	10936	0.67	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares fetal liver, spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
642	5803	10937	0.67	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares fetal liver, spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
645	5806		4.64	0.0E+00	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
652	5813	10949	2.56	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
654	5815	10952	2	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
657	5818	10956	5.7	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
661	5822	10959	0.8	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
661	5822	10960	0.8	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
667	5827	10965	4.66	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
667	5827	10966	4.66	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
673	7896		2.1	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
681	5839	10979	18.62	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nucleosome chromosomal) protein 1 (HMG1) mRNA
685	5843	10982	15.5	0.0E+00	AB029012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
695	5852	10997	3.94	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA
707	5864	11011	7.47	0.0E+00	AA614537.1	EST_HUMAN	np49d01.s1 NCL_CGAP_B1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb-X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
711	5868	11015	5.35	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
711	5868	11016	5.35	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
721	5878	11025	1.28	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF-1) mRNA
727	5883	11031	4.5	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
727	5883	11032	4.5	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
729	5885	11035	8.31	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
735	5891	11043	3.29	0.0E+00	BE241577.1	EST_HUMAN	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) BAYOR-HGSC project-TCAA Homo sapiens cDNA clone TCAAP0779
755	5910	11087	0.87	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
755	5910	11088	0.87	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
758	5913	11071	0.77	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
758	5913	11072	0.77	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
761	5916	11073	2.25	0.0E+00	AB037760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
762	5917	11074	3.68	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
764	7900	11076	4.44	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
765	5919	11077	8.27	0.0E+00	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
769	5923	11081	3.55	0.0E+00	R48915.1	EST_HUMAN	Y69g08.r1 Soares breast 2NBH8t Homo sapiens cDNA clone IMAGE:154046 5'
770	5924	11082	6.85	0.0E+00	6032086	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
779	5933	11081	2.29	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
782	5937	11095	4.63	0.0E+00	7661956	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
783	5947	11107	1.45	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
783	5947	11108	1.45	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
788	5952	11112	1.99	0.0E+00	X89772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
802	5956	11116	2.27	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
802	5956	11117	2.27	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
807	5960	11123	7.36	0.0E+00	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
808	5961		7.7	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
825	5978	11144	1.77	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA

Page 183 of 214  
Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
826	5979	11145	2.22	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
828	5981	11147	2.39	0.0E+00	4557686	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KONE1), mRNA
834	5986	11153	1.75	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MINBH), mRNA, complete cds
834	5986	11154	1.75	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MINBH), mRNA, complete cds
835	5987	11155	0.94	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MINBH), mRNA, complete cds
840	5992	11160	2.02	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
844	5995	11165	1.79	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
844	5995	11166	1.79	0.0E+00	4607600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
851	6002	11177	1.67	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
856	6009	11177	6.75	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
856	6008	11178	6.75	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
856	6007	11179	14.37	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON), mRNA
857	6008	11180	9.8	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
858	6009	11181	12.33	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S5 (RPS5), mRNA
862	6013	11184	1.11	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
862	6013	11185	1.11	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
863	6014	11186	1.69	0.0E+00	AA533272.1	EST_HUMAN	U66607.s1 NCI_CGAP_P110 Homo sapiens cDNA clone IMAGE:997453
863	6014	11187	1.69	0.0E+00	AA533272.1	EST_HUMAN	U66607.s1 NCI_CGAP_P110 Homo sapiens cDNA clone IMAGE:997453
864	6015	11188	6.77	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
868	6019	11189	1.57	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
868	6019	11189	1.57	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
869	6020	11190	1.93	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
869	6020	11191	1.93	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
892	6042	11214	0.99	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
896	6049	11219	1.47	0.0E+00	BE089592.1	EST_HUMAN	GV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
899	6049	11220	1.47	0.0E+00	BE089592.1	EST_HUMAN	GV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
909	6056	11229	3.59	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
918	6067		28.71	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (87kD, ribosomal protein SA) (LAMR1), mRNA
921	6067		23.9	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (87kD, ribosomal protein SA) (LAMR1), mRNA
922	6070	11236	1	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds
923	6071	11237	0.75	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
923	6071	11238	0.75	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
923	6071	11239	0.75	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
924	6072	11240	1.66	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (P14) gene, exons 1-4, complete cds

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
927	6075	11243	4.57	0.0E+00	Z20656.1	NT	Homo sapiens cardiac alpha-myosin heavy chain gene
927	6075	11244	4.57	0.0E+00	Z20656.1	NT	Homo sapiens cardiac alpha-myosin heavy chain gene
947	6095	11262	2.02	0.0E+00	AB023211.1	NT	Homo sapiens mRNA for KIAA0994 protein, partial cds
947	6095	11263	2.02	0.0E+00	AB023211.1	NT	Homo sapiens mRNA for KIAA0994 protein, partial cds
952	6100	11268	1.26	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
953	6101	11269	6.7	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
954	6102	11270	0.79	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
955	6103	11271	2.01	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
955	6103	11272	2.01	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
953	7805	11279	2.13	0.0E+00	A1001948.1	EST_HUMAN	os98e03.s1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:1613404.3
953	7805	11280	2.13	0.0E+00	A1001948.1	EST_HUMAN	os98e03.s1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:1613404.3
965	6112	11282	11.65	0.0E+00	7657266	NT	Homo sapiens KIAA0929 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
976	6122	11282	1.42	0.0E+00	AB030566.1	NT	Homo sapiens mRNA for PSP24, complete cds
984	6130	11298	1.57	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-402 GN0014 Homo sapiens cDNA
984	6130	11299	1.57	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-402 GN0014 Homo sapiens cDNA
984	6130	11300	1.57	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-402 GN0014 Homo sapiens cDNA
985	6131	11301	1.52	0.0E+00	X52207.1	NT	Homo sapiens partial c-igr gene, exons 2 and 3
985	6131	11302	1.52	0.0E+00	X52207.1	NT	Homo sapiens partial c-igr gene, exons 2 and 3
984	6140	11309	5.63	0.0E+00	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL), mRNA
1005	6150	11317	1.56	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1006	6151	11318	37.21	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1007	6151	11318	22.91	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1010	6154		4.51	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1011	6154		9.74	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1015	6158	11324	2.06	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1016	6158	11324	3.94	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1017	6158	11324	3.21	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1018	6159	11325	4.91	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1021	6162	11328	2.38	0.0E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1025	6166	11332	3.53	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1027	6168		4.4	0.0E+00	AA458680.1	EST_HUMAN	aa8q07.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838236.3 similar to SW:PRSB_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8;

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1030	6171	11337	7.44	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1030	6171	11338	7.44	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1031	6172	11339	1.27	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1031	6172	11340	1.27	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1035	6176	11355	2.42	0.0E+00	8922833	NT	Homo sapiens hypothetical protein FLJ111196 (FLJ11196), mRNA
1049	6190	11355	10.11	0.0E+00	4758669	NT	Homo sapiens heat shock 70kD protein 9B (mortalin-2) (HSPA9B) mRNA
1066	6206	11368	2.38	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1066	6206	11368	2.38	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1070	6210	11373	2.8	0.0E+00	8923824	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1070	6210	11373	2.8	0.0E+00	8923824	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1071	6211	11375	58.12	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1073	6213	11375	2.44	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1075	6215	11379	4.37	0.0E+00	5174384	NT	Homo sapiens alkylation repair; alkB homolog (ABH), mRNA
1083	6222	11399	4.61	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1097	6235	11398	2.69	0.0E+00	BE005208.1	EST_HUMAN	MRO-BND115-200300-003-008 BND115 Homo sapiens cDNA
1120	6258	11422	5.21	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1120	6258	11423	5.21	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1133	6270	11433	2.38	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1133	6270	11434	2.38	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1134	6271	11435	20.33	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1136	6273	11437	1.6	0.0E+00	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1139	6276	11440	15.73	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1141	6278	11441	52.48	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1142	6279	11442	5.53	0.0E+00	7657463	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1142	6279	11442	5.53	0.0E+00	7657463	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1146	6282	11446	2.67	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
1147	6283	11447	0.7	0.0E+00	X95826.1	NT	H. sapiens ART4 gene
1147	6283	11448	0.7	0.0E+00	X95826.1	NT	H. sapiens ART4 gene
1148	6284	11449	1.44	0.0E+00	AI147650.1	EST_HUMAN	q622d10.x1 Soares, pregnant uterus NbhPU Homo sapiens cDNA clone IMAGE:16970113
1150	6286	11451	1.59	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1157	6293	11457	1.11	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1157	6293	11458	1.11	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA

Page 188 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1158	6294	11459	0.8	0.0E+00	896844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1170	6305	11471	3.47	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1170	6305	11472	3.47	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1173	6308	11476	1.64	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1180	6315	11484	51.8	0.0E+00	4557987	NT	Homo sapiens keratin 18 (KRT18), mRNA
1184	6328	11495	2.36	0.0E+00	AF073289.1	NT	Homo sapiens Na <sup>+</sup> /H <sup>+</sup> exchanger isoform 2 (NHE2) mRNA, complete cds
1212	6344		1.73	0.0E+00	7657336	NT	Homo sapiens mult. (E. coli) homolog 3 (MLH3), mRNA
1225	6357	11527	1.26	0.0E+00	8922993	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
1228	6361	11531	3.23	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1229	6361	11532	3.23	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1230	6362	11533	5.19	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1231	7911	11534	4.17	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1250	6380	11559	8.44	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1251	6381	11560	1.11	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1261	6390	11568	10.12	0.0E+00	4505740	NT	Homo sapiens prefoldin 4 (PF4D4), mRNA
1270	6399		2.69	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1278	6407	11581	191.34	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
1285	6414	11590	5.41	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSR9) mRNA, complete cds
1291	6420	11594	2.8	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1291	6420	11595	2.8	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1304	6434	11608	2.48	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1304	6434	11609	2.48	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1304	6434	11610	2.48	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1305	6435		2.72	0.0E+00	AF096156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1316	7913	11622	1.16	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1316	7913	11623	1.16	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1321	6450	11629	1.18	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNFG), mRNA
1322	6451	11630	3.29	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173), mRNA
1324	6453	11631	1.01	0.0E+00	5803146	NT	Homo sapiens zinc finger protein 9 (RNFG), mRNA
1325	6464	11632	2.76	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173), mRNA
1327	6456	11634	4.1	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1328	6457	11635	7.17	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1329	6458	11636	4.33	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1330	6459	11637	4.06	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA



Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1330	6459	11638	4.06	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1342	6470	11651	2.07	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1416	6543	11722	0.98	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cyd gene
1422	6549	11730	3.33	0.0E+00	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
1425	6552	11734	1.43	0.0E+00	AJ208756.1	EST_HUMAN	4938506.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:727A1.5 CE14213;
1426	6553	11735	22.77	0.0E+00	6042206	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1435	6562	11745	2.3	0.0E+00	4505846	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1435	6562	11746	2.3	0.0E+00	4505846	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1437	6564	11749	4.16	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1437	6564	11750	4.16	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1440	6567	11762	4.87	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1450	6578	11765	4.23	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-6Glucosyltransferase (alpha1-6Fuct) gene, exon 7
1461	6588	11776	2.18	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1461	6588	11777	2.18	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1466	6593	11781	4.88	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1468	6593	11782	4.88	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1474	6601	11786	2.57	0.0E+00	AL132999.1	NT	Novel human gene on chromosome 20
1475	6602	11787	1.36	0.0E+00	AL137764.1	NT	Novel human gene mapping to chromosome 1
1479	6606	11792	1.8	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1482	6609	11795	6.7	0.0E+00	6012457	NT	Homo sapiens cdcincurth binding protein 1 (KIAA0330), mRNA
1484	6611	11797	1.25	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1484	6611	11798	1.25	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1525	6652	11838	1.35	0.0E+00	7706434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51696), mRNA
1539	6667	11853	1.51	0.0E+00	AW959687.1	EST_HUMAN	EST371757 MAGE sequences, MAGF Homo sapiens cDNA
1540	6668	11854	2.48	0.0E+00	AA481172.1	EST_HUMAN	aa24a03.11 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815116 5'
1546	6674	11858	130.24	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1546	6674	11859	130.24	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1548	6676	11862	1.27	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE sequences, MAGN Homo sapiens cDNA
1548	6676	11863	1.27	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE sequences, MAGN Homo sapiens cDNA
1549	6677	11864	2.41	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1551	6679		2.42	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1552	6581	11868	5.69	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1552	6581	11869	5.69	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1553	6582	11870	2.73	0.0E+00	7662405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1554	6583	11871	7.14	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1560	6589	11876	3.37	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1563	6592	11878	2.36	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1563	6592	11879	2.36	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1564	7920		46.38	0.0E+00	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1565	6593	11880	42.77	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1576	6705	11895	2.22	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1576	6705	11896	2.22	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1578	6707	11897	6.99	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1584	6713		3.79	0.0E+00	D00333.1	NT	human c-yes-2 gene
1593	6722	11912	11.87	0.0E+00	Z83738.1	NT	H. sapiens hH2B/e gene
1594	6723	11913	1.35	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1594	6723	11914	1.35	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1595	6724	11915	7.45	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKG Homo sapiens cDNA clone GKCB0F02 5'
1595	6724	11916	7.45	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKG Homo sapiens cDNA clone GKCB0F02 5'
1698	7921	11919	6.37	0.0E+00	AB040505.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1601	6729	11920	1.64	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1603	6731	11923	6.11	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1603	6731	11924	6.11	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1605	6733	11925	106.24	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1605	6733	11926	106.24	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1607	6735	11928	2.08	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1622	6750	11944	9.74	0.0E+00	H26973.1	EST_HUMAN	yo76c05.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:183848 3'
1630	6769	11954	2.1	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1630	6759	11955	2.1	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1649	6777	11969	1.59	0.0E+00	AW444637.1	EST_HUMAN	UH-B13-ajw-c-04 0-U1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
1678	6807	12004	1.53	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1678	6807	12005	1.53	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1682	6811	12009	2.57	0.0E+00	AI769104.1	EST_HUMAN	wg81b07.x1 Soares NSF_F8_9W_OT_PA_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN ;
1683	6812	12010	1.99	0.0E+00	4758513	NT	Homo sapiens hematopoietic-derived zinc finger protein (HD-ZNF1) mRNA

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1684	6813	12011	2.16	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1687	6816	12014	3.33	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1687	6816	12015	3.33	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1689	6819	12017	46.19	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1690	6819	12018	1	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1694	6823	12021	1.5	0.0E+00	BE222374.1	EST_HUMAN	h11405.x1 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147
1694	6823	12022	1.5	0.0E+00	BE222374.1	EST_HUMAN	MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1696	6824	12024	1.75	0.0E+00	4557610	NT	h11405.x1 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147
1699	6827	12027	5.05	0.0E+00	H30132.1	EST_HUMAN	MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1699	6827	12028	5.05	0.0E+00	H30132.1	EST_HUMAN	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1701	6829	12030	10.76	0.0E+00	Z80780.1	NT	yo59e08.r1 Soares breast 3Nbl-Bst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
1701	6829	12031	10.76	0.0E+00	Z80780.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1704	6832	12031	37.83	0.0E+00	5031748	NT	yo59e08.r1 Soares breast 3Nbl-Bst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
1712	6840	12041	1.57	0.0E+00	AF169983.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1714	6841	12044	4.76	0.0E+00	8923841	NT	H. sapiens H2B/h gene
1717	6844	12047	1.8	0.0E+00	5453855	NT	H. sapiens H2B/h gene
1722	6849	12054	1.39	0.0E+00	4826973	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1728	6855	12061	6.99	0.0E+00	AB026542.1	NT	Homo sapiens WNT16 protein (WNT16) mRNA, complete cds
1730	6857	12075	1.94	0.0E+00	S94400.1	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1744	7824	12075	1.21	0.0E+00	11545911	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1757	6883	12090	2.79	0.0E+00	AF273841.1	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1795	7925	12136	97	0.0E+00	4505718	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1800	6925	12137	2.56	0.0E+00	4557556	NT	TCR zeta [human, Genomic/mRNA, 365 nt, segment 1 of 8]
1800	6925	12137	2.56	0.0E+00	4557556	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1803	6927	12141	2.04	0.0E+00	U63963.1	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1807	6931	12141	1.14	0.0E+00	W76571.1	EST_HUMAN	Homo sapiens E1A binding protein p300 (EP300) mRNA
1808	7928	12148	5.37	0.0E+00	4505332	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1819	6942	12180	21.46	0.0E+00	U14997.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1821	6944	12163	16.15	0.0E+00	AB002331.1	NT	z466g09.r1 Soares fetal heart Nbl-H19W Homo sapiens cDNA clone IMAGE:345864 5'
							Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
							Human ribosomal protein L21 mRNA, complete cds
							Human mRNA for KIAA0333 gene, partial cds

Page 190 of 214  
Table 4  
Single Exon Probes Expressed in BT474

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1822	6945	12164	25.6	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1822	6945	12165	25.6	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1822	6945	12166	25.6	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1836	6958	12181	2.33	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1836	6958	12182	2.33	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1848	6969	12189	4.05	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1848	6969	12190	4.05	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1855	6976	12197	2.57	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1855	6976	12198	2.57	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1859	6979	12200	3.45	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNCB1) mRNA
1859	6979	12201	3.45	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNCB1) mRNA
1860	6980	12202	6.38	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1860	6980	12203	6.38	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1863	6983	12206	4.21	0.0E+00	AW207280.1	EST_HUMAN	UHH-B11-afn-f-07-d-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1863	6983	12207	4.21	0.0E+00	AW207280.1	EST_HUMAN	UHH-B11-afn-f-07-d-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1885	7005	12224	3.11	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1885	7005	12225	3.11	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1901	7020	12240	1.4	0.0E+00	BE006292.1	EST_HUMAN	RC2-BN0126-200300-012-b04 BN0126 Homo sapiens cDNA
1925	7044	12264	1.89	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1925	7044	12265	1.89	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1928	7047	12267	3.05	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1928	7047	12268	3.05	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1933	7052	12274	2.16	0.0E+00	AB037789.1	NT	Homo sapiens mRNA for KIAA1367 protein, partial cds
1936	7055	12283	1.49	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1941	7060	12284	3.37	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1941	7060	12284	3.37	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1944	7082	12286	1.05	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
1946	7084		6.43	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Table 4

## Single Exon Probes Expressed in BT474

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1951	7069		2.25	0.0E+00	M5932.1	NT	Human topoisomerase I pseudogene 1
1952	7930	12293	1.2	0.0E+00	5801905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
1954	7071	12295	1.05	0.0E+00	BE018066.1	EST_HUMAN	b673f11.yt NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048045 5'
1960	7077	12300	1.49	0.0E+00	4809282	NT	Homo sapiens histidine aminotriase (HAL) mRNA
1960	7077	12301	1.49	0.0E+00	4809282	NT	Homo sapiens histidine aminotriase (HAL) mRNA
1971	7088	12315	2.57	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1971	7088	12316	2.57	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1972	7089	12317	10.13	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1972	7089	12318	10.13	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1982	7099	12330	1.53	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0760 protein, partial cds
1982	7099	12331	1.53	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0760 protein, partial cds
1987	7104	12335	1.16	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1987	7104	12336	1.16	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1989	7106	12337	3.18	0.0E+00	AW193024.1	EST_HUMAN	x69801.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879913 3'
1989	7106	12338	3.18	0.0E+00	AW193024.1	EST_HUMAN	x69801.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879913 3'
1990	7107	12339	6.81	0.0E+00	8912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1990	7107	12340	6.81	0.0E+00	8912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1992	7109	12342	1.01	0.0E+00	7662095	NT	Homo sapiens KIAA0408 gene product (KIAA0408), mRNA
1993	7110	12343	1.9	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1994	7111	12344	1.53	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1994	7111	12345	1.53	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
2001	7118	12354	5.36	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
2016	7133	12370	1.75	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2016	7133	12371	1.75	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2045	7161	12400	1.13	0.0E+00	7708742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2049	7165	12404	23.48	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2049	7165	12405	23.48	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2051	7167	12406	1.37	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (FX) mRNA
2052	7168	12407	2.16	0.0E+00	BF207988.1	EST_HUMAN	601861974F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081483 5'
2053	7169	12408	3.83	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2055	7171	12410	1.56	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2055	7171	12411	1.56	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2057	7173		1.8	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA

Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2059	7175		1.25	0.0E+00	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2060	7176	12414	1.76	0.0E+00	Z42399.1	EST_HUMAN	HSC01C021 normalized Infant brain cDNA Homo sapiens cDNA clone c-01c02
2062	7178		1.1	0.0E+00	A1244247.1	EST_HUMAN	q980708.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element
2066	7182	12422	2.39	0.0E+00	BE877225.1	EST_HUMAN	G01465146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2068	7184	12424	2.08	0.0E+00	BF315325.1	EST_HUMAN	G01902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2068	7184	12425	2.08	0.0E+00	BF315325.1	EST_HUMAN	G01902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2073	7189	12431	2.66	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2073	7189	12432	2.66	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2079	7195	12439	2.02	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2079	7195	12440	2.02	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2080	7196	12441	1.02	0.0E+00	AJ297705.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 1
2083	7199	12444	1.6	0.0E+00	4758480	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2103	7218		3.19	0.0E+00	BE767964.1	EST_HUMAN	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2104	7219		1.48	0.0E+00	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLRST) gene, exon 6 and complete cds
2106	7221	12465	6.48	0.0E+00	BF027562.1	EST_HUMAN	G01672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2107	7222	12466	1.85	0.0E+00	BE072624.1	EST_HUMAN	PM0-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2109	7224	12467	2.8	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2112	7227	12469	6.06	0.0E+00	AW762708.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2113	7228	12470	1.02	0.0E+00	L76827.1	NT	Homo sapiens metabotropic glutamate receptor 1 alpha (mGluR1alpha) mRNA, complete cds
2115	7230	12472	10.62	0.0E+00	A1904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2115	7230	12473	10.62	0.0E+00	A1904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2161	7274		2.02	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3' end
2166	7281	12527	1.29	0.0E+00	BE274696.1	EST_HUMAN	G01122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345688 5'
2170	7283	12530	1.18	0.0E+00	D87885.1	NT	Human mRNA for KIAA0244 gene, partial cds
2171	7284	12531	47.76	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2171	7284	12532	47.76	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2173	7286	12534	202.57	0.0E+00	AA931691.1	EST_HUMAN	cc32e01.st NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567896 3'
2176	7288		1.32	0.0E+00	M19828.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 29
2178	7291	12538	8.02	0.0E+00	BF344434.1	EST_HUMAN	G02014829F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150734 5'
2179	7292	12539	143.71	0.0E+00	BE748899.1	EST_HUMAN	G01572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3639012 3'
2183	7296	12543	2.92	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2183	7296	12544	2.92	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA

Page 193 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2188	7305	12547	7.23	0.0E+00	BF313617.1	EST_HUMAN	601900261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126222 5'
2189	7301	12550	2.24	0.0E+00	BE018750.1	EST_HUMAN	bb84e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TRQ15170 Q15170 TRANSCRIPTION FACTOR S-I-RELATED PROTEIN ;
2190	7302	12551	2.98	0.0E+00	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_Nb1PU Homo sapiens cDNA clone IMAGE:466540 3' similar to gb:X65857 cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2190	7302	12552	2.98	0.0E+00	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_Nb1PU Homo sapiens cDNA clone IMAGE:466540 3' similar to gb:X65857 cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2197	7309	12559	3.51	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2197	7309	12560	3.51	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2198	7310	12562	3.77	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2203	7315	12572	2.39	0.0E+00	U36264.1	EST_HUMAN	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2203	7315	12572	6.18	0.0E+00	BE897487.1	EST_HUMAN	Human beta-prime-adaptin (BAM22) gene, exon 16
2222	7334	12588	6.73	0.0E+00	4557556	NT	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
2227	7339	12593	1.81	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2233	7345	12600	4.45	0.0E+00	BE895281.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5'
2237	7349	12604	2.4	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2237	7349	12605	2.4	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2239	7350	12607	2.92	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2274	7384	12632	3.79	0.0E+00	BF344756.1	EST_HUMAN	602014009F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4149770 5'
2274	7384	12633	3.79	0.0E+00	BF344756.1	EST_HUMAN	602014009F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4149770 5'
2276	7386	12635	3.08	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 8 (DEF6), mRNA
2278	7388	12636	3.08	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 8 (DEF6), mRNA
2277	7387	12637	2.3	0.0E+00	A1076404.1	EST_HUMAN	6009c07.x1 Soares_fetal_liver_spleen_INF1S_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2280	7390	12640	3.56	0.0E+00	AA428001.1	EST_HUMAN	zv78a11.1 Soares_fetal_liver_spleen_INF1S_S1 Homo sapiens cDNA clone IMAGE:759740 5'
2280	7390	12641	3.56	0.0E+00	AA428001.1	EST_HUMAN	zv78a11.1 Soares_fetal_liver_spleen_INF1S_S1 Homo sapiens cDNA clone IMAGE:759740 5'
2282	7392	12643	2.98	0.0E+00	BF347036.1	EST_HUMAN	602021846F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157339 5'
2283	6880	11867	1.1	0.0E+00	M18768.1	NT	Human T-cell receptor gamma chain VJCI-CII region mRNA, complete cds
2288	7397	12649	1.03	0.0E+00	LD2840.1	NT	Homo sapiens potassium channel Kv2.1 mRNA, complete cds
2289	7398	12650	1.01	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2289	7398	12651	1.01	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2290	7399	12652	1.23	0.0E+00	6325466	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2297	7406	12658	2.86	0.0E+00	BE676095.1	EST_HUMAN	7722a02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3285370 3' similar to TR:O94939 O94939 KIAA0857 PROTEIN ;

Page 194 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2300	7409	12660	11.14	0.0E+00	AF044571.1	NT	Homo sapiens phosphorylase kinase alpha subunit (PHKA2) gene, exon 32
2301	7410	12661	1.94	0.0E+00	AI625642.1	EST_HUMAN	U67608.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2283182 3'
2303	7412	12662	1.89	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
2306	7415	12664	3.71	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2306	7415	12665	3.71	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2309	7418	12668	2.32	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2309	7418	12669	2.32	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2316	7424	12674	1.92	0.0E+00	7662007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2320	7428	12680	1.25	0.0E+00	D83778.1	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2320	7428	12681	1.25	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2328	7436	12688	1.8	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2332	7439	12692	2.97	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2333	7440	12693	70.49	0.0E+00	BE794028.1	EST_HUMAN	601586843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2334	7441	12693	1	0.0E+00	AW867076.1	EST_HUMAN	MR1-SN0033-120-400-002-a04 SN0033 Homo sapiens cDNA
2335	7442	12694	6.53	0.0E+00	7662017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2336	7443	12695	1.52	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2336	7443	12696	1.52	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2337	7444						Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2339	7446	12698	2.39	0.0E+00	AF280107.1	NT	4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2339	7446	12699	19.43	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2339	7446	12699	19.43	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2340	7447	12701	1.58	0.0E+00	8923089	NT	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2340	7447	12701	1.58	0.0E+00	8923089	NT	Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2346	7465		4.27	0.0E+00	BE814424.1	EST_HUMAN	MR0-BN0070-090600-029-d12 BN0070 Homo sapiens cDNA
2392	7498		3.25	0.0E+00	AI042035.1	EST_HUMAN	ox60x02.x1 Soares_NhrIMP_u_S1 Homo sapiens cDNA clone IMAGE:1860883 3' similar to TR:O08662
2394	7500	12751	4.38	0.0E+00	8923620	NT	O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE ;
2396	7502	12752	1	0.0E+00	AW303988.1	EST_HUMAN	xx15807.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR:O54924
2398	7504		3.28	0.0E+00	BE895605.1	EST_HUMAN	O54924 EXO84 ;
2410	7516		4.98	0.0E+00	AB005622.1	EST_HUMAN	601437608FT NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2413	7519	12769	5.88	0.0E+00	6006002	NT	AB005622 HeLa cDNA (T.Noma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
							Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA



Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2417	7522	12773	1.61	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2417	7522	12774	1.61	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2425	7530	12783	1.04	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2429	7533	12786	1.5	0.0E+00	BF346274.1	EST_HUMAN	G02018058F1 NCL CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4153670 5'
2436	7540	12794	2.44	0.0E+00	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2439	7543	12796	1.13	0.0E+00	BE831003.1	EST_HUMAN	CM0-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2439	7543	12797	1.13	0.0E+00	BE831003.1	EST_HUMAN	CM0-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2444	7548	12801	37.91	0.0E+00	BF569144.1	EST_HUMAN	G02184598T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2451	7555	12807	4.45	0.0E+00	AW468922.1	EST_HUMAN	ha04h04.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'
2453	7557	12808	2.12	0.0E+00	AW501010.1	EST_HUMAN	UI-HF-BP0p-ais-c-07-O-UI.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2476	7580		1.9	0.0E+00	AW813953.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2480	7585	12835	55.02	0.0E+00	BE795542.1	EST_HUMAN	G01592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2481	7592	12866	1.18	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2482	7588	12836	2.07	0.0E+00	BF509482.1	EST_HUMAN	UI-H-B14-azb-b-08-O-UI.s1 NCL CGAP_Sub88 Homo sapiens cDNA clone IMAGE:3086535 3'
2485	7589	12838	1.23	0.0E+00	Z32684.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2487	7591		2.28	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mRNA
2490	7594	12842	1.61	0.0E+00	BE910378.1	EST_HUMAN	G015033356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2491	7595	12843	1.54	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2492	7598	12844	5.51	0.0E+00	BE150865.1	EST_HUMAN	RC4-HT0276-160200-013-405 HT0276 Homo sapiens cDNA
2493	7597	12845	3.17	0.0E+00	8923340	NT	Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA
2494	7598	12846	10.75	0.0E+00	U93236.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2499	7603	12861	10.62	0.0E+00	BE886400.1	EST_HUMAN	G01508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909868 5'
2504	7607	12857	3.04	0.0E+00	BE875511.1	EST_HUMAN	G01498241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2504	7607	12858	3.04	0.0E+00	BE875511.1	EST_HUMAN	G01498241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2505	7608	12859	1.27	0.0E+00	AF114027.1	EST_HUMAN	AF114027 Homo sapiens lung fetus Homo sapiens cDNA clone ESF6
2507	7610	12862	1.44	0.0E+00	AF245505.1	NT	Homo sapiens adiclin mRNA, complete cds
2522	7626	12870	1.17	0.0E+00	BE536921.1	EST_HUMAN	G01064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2526	7629	12876	11.25	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2526	7629	12877	11.25	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2527	7630	12878	1.85	0.0E+00	BE292896.1	EST_HUMAN	G01105312F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2987956 5'
2527	7630	12879	1.85	0.0E+00	BE292896.1	EST_HUMAN	G01105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987956 5'
2530	7633	12881	4.83	0.0E+00	AF245505.1	NT	Homo sapiens adiclin mRNA, complete cds
2581	7878	12817	3.58	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2581	7878	12818	3.58	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds

Page 196 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2562	7663		1.77	0.0E+00	BF513835.1	EST_HUMAN	UI-H-BW1-amp-f-12-0-JL1s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2568	7669	12924	1.94	0.0E+00	BF672818.1	EST_HUMAN	G02152653F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293612 5'
2570	7671		1.23	0.0E+00	BE616695.1	EST_HUMAN	G01279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621786 5'
2576	7676	12930	4.12	0.0E+00	AB037742.1	NT	Homo sapiens mRNA for KIAA1321 protein, partial cds
2577	7677	12931	0.95	0.0E+00	AI571737.1	EST_HUMAN	tn19b08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2168055 3' similar to gbL20977 CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN); Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 28kD (TAF2)
2578	7678	12932	2.82	0.0E+00	5032150	NT	mRNA
2580	7681	12936	3.56	0.0E+00	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2581	7682	12937	1.35	0.0E+00	BE795445.1	EST_HUMAN	G01590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2581	7682	12938	1.35	0.0E+00	BE795445.1	EST_HUMAN	G01590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2591	7692		13.31	0.0E+00	BE792472.1	EST_HUMAN	G01584630F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'
2593	7694	12948	1.19	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
2600	7700	12955	3.59	0.0E+00	4504686	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2602	7946	12958	0.99	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
2608	7707	12962	3.82	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2611	7710	12963	1.64	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
2613	7712	12965	1.12	0.0E+00	AU133385.1	EST_HUMAN	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001964 5'
2614	7713	12966	1.11	0.0E+00	M69228.1	NT	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds
2616	7715	12968	3.79	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2616	7715	12969	3.79	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2619	7718	12972	1.43	0.0E+00	AW887015.1	EST_HUMAN	RC1-OT0086-220300-011-407 OT0086 Homo sapiens cDNA
2622	7721	12975	1.95	0.0E+00	BF000018.1	EST_HUMAN	7h15h05.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316089 3'
2623	7722	12976	4.51	0.0E+00	BE383165.1	EST_HUMAN	G01298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2624	7723		2.17	0.0E+00	BE531263.1	EST_HUMAN	G01278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610287 5'
2649	7747	12998	1.33	0.0E+00	8922843	NT	Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA
2659	7755	13006	1.25	0.0E+00	AB037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
2684	7781		24.59	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2685	7782	13030	43.93	0.0E+00	BE794884.1	EST_HUMAN	G01589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2690	7787	13037	4.97	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2692	7789	13039	1.58	0.0E+00	7669517	NT	Homo sapiens neuregulin 1 (NRG1), transcript variant SMD5, mRNA
2693	7790	13040	1.85	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2694	7791	13041	2.6	0.0E+00	AB051826.1	NT	Homo sapiens hG28K mRNA for GTP-binding protein like 1, complete cds

Page 197 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2700	7798	13047	90.08	0.0E+00	BE796376.1	EST_HUMAN	601591991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2701	7797	13048	1.94	0.0E+00	BF680832.1	EST_HUMAN	602155923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297132 5'
2704	7949	13052	75.81	0.0E+00	BE563433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'
2705	7800		2.71	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE08 5'
2707	7802	13055	1.9	0.0E+00	5174488	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2707	7802	13058	1.9	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2708	7803	13057	1.94	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2708	7803	13058	1.94	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2709	7804	13059	9.14	0.0E+00	AF290195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2710	7805		61.45	0.0E+00	AV651066.1	EST_HUMAN	AV651066 GLC Homo sapiens cDNA clone GLCCLD07 3'
2711	7808	13080	2.74	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b38 TN0141 Homo sapiens cDNA
2711	7808	13061	2.74	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b38 TN0141 Homo sapiens cDNA
2715	7810	13084	6.04	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDRT1) mRNA
2715	7810	13085	6.04	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDRT1) mRNA
2719	7814	13070	37.71	0.0E+00	BE747193.1	EST_HUMAN	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2730	7825		1.28	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2731	7826	13081	2.6	0.0E+00	BF514110.1	EST_HUMAN	UJ-H-BW1-arnw-e-07-0-UI st NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2742	7836	13089	1.66	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2743	7837	13091	1.66	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2743	7837	13091	2.45	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
2749	7843	13099	1.65	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2752	7846	13101	37.83	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTGCCA03 5'
2752	7846	13102	37.83	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTGCCA03 5'
2754	7848		14.98	0.0E+00	AI879163.1	EST_HUMAN	au55d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW:R13A, HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
2757	7851	13107	2.14	0.0E+00	BF530861.1	EST_HUMAN	602071957F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4214679 5'
2758	7852	13108	147.71	0.0E+00	BE872768.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5'
2760	7854	13109	3.95	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2760	7854	13110	3.85	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2761	7855	13111	128.52	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860806 5'
2761	7855	13112	128.52	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860806 5'
2767	5378	10519	3.63	0.0E+00	S76830.1	NT	glycoprotein D-Duffy group antigen [human, blood, Genomic DNA, 3068 nt]
2770	7862		2.78	0.0E+00	AB033281.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2776	5888	11040	3.94	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds

Page 198 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2776	5888	11041	3.94	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2780	6182	11347	2.85	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2780	6182	11348	2.85	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2797	7954	13120	2.95	0.0E+00	X85980.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2798	7955		1.43	0.0E+00	AF068624.1	NT	Homo sapiens 5-aminolevulinic acid synthase 2 (ALAS2) gene, complete cds
2800	7957		1.28	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2807	7963		1.07	0.0E+00	AJ238852.1	NT	Homo sapiens partial rpl3 gene for ribosomal protein L3, U82 snoRNA, U83a snoRNA and U83b snoRNA genes
2808	7964	13125	2.44	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2812	7966	13128	5.27	0.0E+00	M80902.1	NT	Human AHNK nucleoprotein mRNA, 5' and
2815	7971	13130	1.01	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2815	7971	13131	1.01	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2817	7973		1.91	0.0E+00	X73428.1	NT	H. sapiens lds gene for HLH type transcription factor
2819	7975		2.62	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
2820	7976	13134	1.39	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2820	7976	13135	1.39	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2820	7976	13136	1.39	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2826	7981	13142	45.48	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2826	7981	13143	45.48	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2830	7985	13146	3.23	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2831	7986		5.71	0.0E+00	Y10658.1	NT	H. sapiens mRNA for nuclear DNA helicase II
2832	7987		1.11	0.0E+00	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2833	7988	13147	89.98	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2833	7988	13148	89.98	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2846	8001	13161	2.44	0.0E+00	4507280	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2849	8004	13165	1.2	0.0E+00	AL047599.1	EST_HUMAN	DKFZp566G0621_j1 586 (synonym: huter) Homo sapiens cDNA clone DKFZp566G0621
2850	8005	13166	0.93	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2850	8005	13167	0.93	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2851	8006		1.55	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanocyte-associated) (CSPG4), mRNA
2854	8009	13169	5.69	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2854	8009	13170	5.69	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2856	8014	13178	0.82	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

Page 199 of 214  
Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2859	8014	13179	0.82	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2862	8017	13183	2	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2862	8017	13184	2	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2869	8023		3.71	0.0E+00	Y19210.1	NT	Homo sapiens Hb5 gene for hair keratin, exons 1 to 9
2872	8028	13193	1.05	0.0E+00	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2874	8028	13196	42.84	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2875	8029	13197	0.98	0.0E+00	A1561002.1	EST_HUMAN	tn18d07.x1 NCI_CGAP_Bn26 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2875	8029	13198	0.98	0.0E+00	A1561002.1	EST_HUMAN	tn18d07.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2876	8030	13199	1.47	0.0E+00	P52740	SWISSPROT	O16247 F44E7.2 PROTEIN. ;
2877	8031	13200	0.95	0.0E+00	AF152338.1	NT	ZINC FINGER PROTEIN 132
2883	8047	13212	1.7	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2883	8047	13213	1.7	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2894	8048	13214	5.83	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2894	8048	13215	5.83	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2897	8051	13218	3.55	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2897	8051	13219	3.55	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2898	8052	13220	3.81	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax) (Drosophila) homolog; translocated to, 4 (MLLT4) mRNA
2898	8052	13221	3.81	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax) (Drosophila) homolog; translocated to, 4 (MLLT4) mRNA
2903	8056	13225	1.18	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
2903	8056	13226	1.18	0.0E+00	BF110702.1	EST_HUMAN	Q9VLN1 CG17293 PROTEIN. ;
2911	8065	13237	2.63	0.0E+00	4505084	NT	7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
2911	8065	13238	2.63	0.0E+00	4505084	NT	Q9VLN1 CG17293 PROTEIN. ;
2920	8074	13244	1.53	0.0E+00	4758827	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2921	8075		0.99	0.0E+00	X98494.1	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2924	8078	13247	1.5	0.0E+00	AB033034.1	NT	Homo sapiens neurexin III (NFXN3) mRNA
2927	8081	13249	8.58	0.0E+00	AF106276.1	NT	H. sapiens mRNA for M phase phosphoprotein 10
2943	8097		0.98	0.0E+00	A1149880.1	EST_HUMAN	Homo sapiens mRNA for KIAA1208 protein, partial cds
2951	8105	13270	2.42	0.0E+00	AB004884.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
							qf43f09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
							Homo sapiens mRNA for PKU-alpha, partial cds

Page 200 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2962	8116	13278	1.8	0.0E+00	7662273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
2963	8117	13279	2.04	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2963	8117	13280	2.04	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2967	8121	13285	1.1	0.0E+00	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
2975	8129	13292	0.78	0.0E+00	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2975	8129	13293	0.76	0.0E+00	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2998	8153		0.67	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2999	8154	13313	1.15	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
3009	8183	13320	0.65	0.0E+00	4506882	NT	Homo sapiens semenogelin I (SEMG1) mRNA
3011	8166	13322	1.09	0.0E+00	AW976286.1	EST_HUMAN	EST388375 IMAGE resequences, MAGN Homo sapiens cDNA
3016	8170		3.92	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3019	8173	13330	6.99	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA7A), mRNA
3019	8173	13331	6.99	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA7A), mRNA
3021	8175		6.28	0.0E+00	AL359403.1	NT	Isform 2 of a novel human mRNA from chromosome 22
3025	8179	13335	2.77	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
3028	8182		1.92	0.0E+00	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds, and L-type calcium channel a7
3048	8202	13358	3.16	0.0E+00	X03529.1	NT	Human germline gene 18.1 for Ig lambda L-chain C region (IgL-C18.1)
3054	8207		1.54	0.0E+00	AF198355.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3058	8211	13365	1.43	0.0E+00	AF084585.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3082	8235	13385	4.26	0.0E+00	AF263208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3083	8236	13386	5.02	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3088	8241	13390	3.23	0.0E+00	7682139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3089	8242	13391	1.32	0.0E+00	AF042076.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3119	8271	13427	3.27	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3129	8280	13436	50.99	0.0E+00	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds
3132	8283	13439	1.16	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3132	8283	13440	1.16	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3139	8280	13447	22.17	0.0E+00	T94870.1	EST_HUMAN	y63263.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:329539
3155	8306	13466	1.16	0.0E+00	BF243336.1	EST_HUMAN	601878507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3157	8308	13467	1.08	0.0E+00	A198086.1	EST_HUMAN	wa12h10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2516803 3'

Page 201 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3162	8313	13474	4.29	0.0E+00	X8922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3162	8313	13475	4.29	0.0E+00	X8922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3164	8315	13477	1.37	0.0E+00	AI665950.1	EST_HUMAN	tu38g09.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW-RASD_DICD1
3176	8327	13490	1.73	0.0E+00	4759827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3176	8327	13491	1.73	0.0E+00	4759827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3183	8334	13497	8.16	0.0E+00	4504658	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3202	8353	13515	6.26	0.0E+00	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3205	8356	13517	2.68	0.0E+00	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3211	8362	13525	0.79	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3211	8362	13526	0.79	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3213	8364	13527	34.87	0.0E+00	AA774783.1	EST_HUMAN	aa87b11.st Stratogene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3221	8372	13536	5.67	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3221	8372	13536	5.67	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3231	8391	13541	1.18	0.0E+00	4557550	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3236	8386	13548	0.92	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3244	8394	13556					Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
3247	8397	13559	1.1	0.0E+00	AF019413.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3250	8400	13561	4.03	0.0E+00	AF055084.1	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3250	8400	13562	1.25	0.0E+00	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3258	10304	13569	1.25	0.0E+00	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3268	10304	13570	2.51	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3274	8423	13584	2.51	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3275	8424	13585	3.1	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3295	8442	13604	1.83	0.0E+00	6923624	NT	Homo sapiens hypohelical protein FLJ20695 (FLJ20695), mRNA
3295	8442	13604	0.67	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3305	8452	13614					ts8808.x2 NCI CGAP_Par1 Homo sapiens cDNA clone IMAGE:2222535 3' similar to SW:RL11_RAT
3313	8460	13622	4.47	0.0E+00	AI689294.1	EST_HUMAN	P25121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element;
3313	8460	13623	2.76	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3314	8461	13624	2.76	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3314	8461	13624	1.06	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA
3314	8461	13625	1.06	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA

Page 202 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3317	8464	13627	2.12	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3317	8464	13628	2.12	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3320	8467	13630	10.5	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3322	8469	13632	1.76	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
3326	8475	13638	0.62	0.0E+00	BE779039.1	EST_HUMAN	601404895F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868248 5'
3339	8485	13651	0.74	0.0E+00	AI632569.1	EST_HUMAN	wb10104.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q91929 Q91929
3377	8522	13686	6.95	0.0E+00	AU123664.1	EST_HUMAN	ZINC FINGER PROTEIN ;
3384	8528	13689	0.98	0.0E+00	7363436	NT	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM2000735 5'
3384	8528	13690	0.98	0.0E+00	7363436	NT	Homo sapiens cytokine receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3387	8531	13692	1.99	0.0E+00	7706239	NT	Homo sapiens cytokine receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3388	8632	13693	1.14	0.0E+00	AF211188.1	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
3393	8637	13701	1.12	0.0E+00	AW867015.1	EST_HUMAN	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1I) mRNA, complete cds
3408	8549	13707	1.44	0.0E+00	7662401	NT	MR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3406	8549	13708	1.44	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3407	8550	13709	1.16	0.0E+00	4502398	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3409	8552	13710	1.95	0.0E+00	5803067	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3418	7790	13040	1.48	0.0E+00	AF110763.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3423	8565	13723	1.95	0.0E+00	7657038	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3426	8568	13727	1.19	0.0E+00	AJ277276.1	NT	Homo sapiens death receptor 6 (DR6), mRNA
3426	8568	13728	1.19	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for tapa-2 (tapa gene)
3427	8569	13729	4.86	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and IncA, IncB, and IncC
3429	8571	13731	1.17	0.0E+00	7427522	NT	Incompatibility determinants
3437	8579	13738	4.18	0.0E+00	AI935159.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
3437	8579	13739	4.18	0.0E+00	AI935159.1	EST_HUMAN	wb14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634
3441	8583	13744	2.5	0.0E+00	AJ276120.1	NT	wb14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634
3447	8589	13752	4.5	0.0E+00	6552332	NT	NEURAL CELL ADHESION MOLECULE ;
3447	8589	13753	4.5	0.0E+00	6552332	NT	NEURAL CELL ADHESION MOLECULE ;
3453	8595	13759	1.7	0.0E+00	MI14123.1	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
							Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
							Human endogenous retrovirus HERV-K10



Page 203 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3458	8600	13764	5.67	0.0E+00	U43293.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3463	8605	13768	0.96	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3463	8605	13769	0.96	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3467	8609	13774	2.45	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3467	8609	13775	2.45	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3474	8616	13783	0.97	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3479	8620	13785	1.12	0.0E+00	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
3481	8622	13787	1.1	0.0E+00	AA626677.1	EST_HUMAN	ab51112.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3481	8622	13788	1.1	0.0E+00	AA626677.1	EST_HUMAN	ab51112.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3481	8622	13789	1.1	0.0E+00	AA626677.1	EST_HUMAN	ab51112.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3485	8626	13793	1.02	0.0E+00	4508028	NT	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45) mRNA
3488	8629	13795	2.4	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3488	8629	13796	2.4	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3492	8633	13800	0.88	0.0E+00	4826795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNK2) mRNA
3495	8636	13803	1.52	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3499	8640	13806	0.62	0.0E+00	A1384007.1	EST_HUMAN	tes35g12.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:000498
3502	8643	13809	1.25	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
3519	8660	13827	0.77	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3519	8660	13828	0.77	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3526	8668	13834	1.13	0.0E+00	AR029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
3528	8670	13835	1.29	0.0E+00	AV701869.1	EST_HUMAN	AV701869 ADB Homo sapiens cDNA clone ADBDAH08 5'
3529	8671	13836	0.87	0.0E+00	4508884	NT	Homo sapiens semenogelin II (SEMG2) mRNA
3531	8673	13836	2.24	0.0E+00	AF078868.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3539	8681	13844	0.95	0.0E+00	AL133204.1	NT	Novel human gene mapping to chromosome X
3541	8682	13845	1.16	0.0E+00	AB040809.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3551	8692	13854	2.08	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
3561	8702	13862	1.08	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3561	8702	13863	1.08	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3562	8703		1.39	0.0E+00	AI081907.1	EST_HUMAN	α77c11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1662356 3' similar to WP.T19B4.4 CE13742;
3584	8705	13866	1.09	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3599	8710		4.53	0.0E+00	AW852217.1	EST_HUMAN	QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA

Page 204 of 214  
Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3576	8717		0.92	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
3577	8718	13875	6.8	0.0E+00	BF676393.1	EST_HUMAN	602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248596 5'
3588	8728	13885	1.05	0.0E+00	AW693767.1	EST_HUMAN	QVQ-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA
3598	8737	13890	1.23	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3598	8737	13891	1.23	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3599	8738		1.31	0.0E+00	4826967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3601	8740	13893	0.72	0.0E+00	AW664693.1	EST_HUMAN	h84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3601	8740	13894	0.72	0.0E+00	AW664693.1	EST_HUMAN	h84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3603	8742	13896	0.71	0.0E+00	4826763	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3605	8744	13899	1.06	0.0E+00	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3610	8749	13905	1.19	0.0E+00	4557752	NT	Homo sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA
3610	8749	13906	1.19	0.0E+00	4557752	NT	Homo sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA
3625	8764	13919	2.89	0.0E+00	D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3628	8767		39.83	0.0E+00	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3644	8783	13937	4.72	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3648	8785	13939	1.12	0.0E+00	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3648	8787	13940	4.08	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3648	8787	13941	4.08	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3657	8796	13951	1.59	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3657	8796	13952	1.59	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3680	8799	13955	1.22	0.0E+00	AW851714.1	EST_HUMAN	MR2-CT0222-281099-005-e05 CT0222 Homo sapiens cDNA
3682	8801	13957	2.19	0.0E+00	5729328	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3684	8803	13959	1.08	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
3686	8805	13961	1.62	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3688	8807	13963	1.15	0.0E+00	7662237	NT	Homo sapiens KIAA0870 protein/acinus (KIAA0870), mRNA
3688	8807	13964	1.15	0.0E+00	7662237	NT	Homo sapiens KIAA0870 protein/acinus (KIAA0870), mRNA
3682	8821	13976	4.6	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BW0-ajs-e-12-0-UI-st NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3682	8821	13977	4.6	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BW0-ajs-e-12-0-UI-st NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3710	8848	14002	1	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen at chain, exon 6
3711	8849	14003	0.9	0.0E+00	AA463659.1	EST_HUMAN	aa08g01.r1 Soares_NhlhMPV_S1 Homo sapiens cDNA clone IMAGE:812486 5' similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIB4, [1];
3716	8854	14008	1.5	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3719	8857	14010	3.8	0.0E+00	7657466	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3728	8865	14019	0.92	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3740	8878	14029	5.49	0.0E+00	7652183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3743	8881	14032	35.82	0.0E+00	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3751	8888	14038	1.22	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3751	8888	14039	1.22	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3798	8935		0.95	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3799	8936	14082	2.6	0.0E+00	AF179733.1	NT	Pan troglodytes difactory receptor (PTR208) gene, partial cds
3802	8939	14086	2.11	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3802	8939	14087	2.11	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3803	8940	14088	1.31	0.0E+00	AF020091.1	NT	Homo sapiens smooth muscle myosin heavy chain SMT mRNA, alternatively spliced, partial cds
3807	8944	14083	1.23	0.0E+00	4759011	NT	Homo sapiens RAB9, member RAS oncogene family (RAB9) mRNA
3810	8947		1.20	0.0E+00	AF152496.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3811	8948	14096	3.81	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DP1) (DSP) mRNA
3814	8951	14099	20.71	0.0E+00	S7885.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds
3816	8953	14101	2.23	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3817	8954	14102	0.95	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3820	8957	14104	0.95	0.0E+00	AF098601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3820	8957	14105	0.93	0.0E+00	AF098601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3825	8961	14110	0.93	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3825	8961	14111	0.93	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3828	8964	14115	0.7	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3833	8969	14123	6.36	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (XORF5) mRNA
3833	8969	14124	6.36	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (XORF5) mRNA
3835	8971	14127	4.16	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3836	8972	14128	0.87	0.0E+00	AF14486.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3839	8975	14130	1.24	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3842	8978	14133	0.91	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3843	8979	14134	2.52	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3845	8981	14136	0.6	0.0E+00	AF099117.1	NT	Homo sapiens amphiphysin gene, partial cds
3853	8989	14145	2.75	0.0E+00	AI864727.1	EST_HUMAN	wk01f01.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:O43340
3856	8992	14149	13.45	0.0E+00	4508742	NT	O43340 R28830_2; contains element PTR7 repetitive element;
3860	8996	14153	1.84	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
							DKFZ434N0413_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZ434N0413 5'

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3864	9000	14157	2.4	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3864	9000	14158	2.4	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3866	9002	14160	2.09	0.0E+00	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3868	9004		1.7	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3872	9008	14164	1.22	0.0E+00	AF149412.1	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3881	9017	14174	1.65	0.0E+00	4508758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
3885	9021	14178	2.19	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
3890	9026	14184	3.22	0.0E+00	BF355295.1	EST_HUMAN	RC3-HIT0860-170800-011-a12 HIT0860 Homo sapiens cDNA
3891	9027	14185	2.92	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5
3891	9027	14186	2.92	0.0E+00	AW888221.1	EST_HUMAN	Matrix remodeling associated gene 5
3899	9035	14194	1.69	0.0E+00	AF129533.1	NT	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5
3902	9038	14197	0.93	0.0E+00	U86281.1	NT	Matrix remodeling associated gene 5
3902	9038	14198	0.93	0.0E+00	U86281.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
3905	9041	14201	3.91	0.0E+00	BE378602.1	EST_HUMAN	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3913	9049	14208	1.33	0.0E+00	AW680740.1	EST_HUMAN	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3948	9083	14235	4.18	0.0E+00	AF116195.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3948	9083	14236	4.18	0.0E+00	AF116195.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3959	9094		3.65	0.0E+00	M23910.1	NT	601236966F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3608800 5'
3962	9097		5.73	0.0E+00	AL163303.2	NT	PM3-L70031-100100-003-H09 L70031 Homo sapiens cDNA
3972	9106	14254	2.97	0.0E+00	AL163284.2	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3980	9114	14262	2.12	0.0E+00	AL163285.2	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3983	9127		79.42	0.0E+00	4503470	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3997	9131		1.29	0.0E+00	AI857076.1	EST_HUMAN	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
4000	9133	14277	2.32	0.0E+00	U03366.1	NT	Homo sapiens chromosome 21 segment HS21C103
4020	9152	14293	6.2	0.0E+00	AB015610.1	NT	Homo sapiens chromosome 21 segment HS21C084
4029	9160		3.39	0.0E+00	AJ238617.1	NT	Homo sapiens chromosome 21 segment HS21C068
4041	9172	14313	2.42	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4042	9173	14314	2.68	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
4042	9173	14315	2.68	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
4049	9180	14321	7.15	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4049	9180	14322	7.15	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4061	9192	14333	0.87	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
4066	9186	14335	4.93	0.0E+00	4885306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4067	9197	14336	1.34	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4070	9200	14337	7.7	0.0E+00	11419297	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4071	9201	14338	4.26	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4078	9208	14345	3.09	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4087	9270	11433	1.6	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4087	6270	11434	1.6	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4091	9220	14356	1.34	0.0E+00	4503864	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4091	9220	14357	1.34	0.0E+00	4503864	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4094	9223	14359	1.34	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4094	9223	14360	1.34	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4098	9227	14363	0.9	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4104	9233	14370	4.5	0.0E+00	A1982597.1	EST_HUMAN	wu04d04.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4104	9233	14371	4.5	0.0E+00	A1982597.1	EST_HUMAN	wu04d04.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4107	9235	14373	1.33	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4107	9235	14374	1.33	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4112	9240		3.99	0.0E+00	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867690 5'
4117	9245	14381	4.44	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4117	9245	14382	4.44	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4119	9247	14384	0.92	0.0E+00	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
4120	9248	14385	3.12	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4128	9256		5.44	0.0E+00	AW675599.1	EST_HUMAN	ba51104.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095 3' similar to SW:TH12_BOVIN
4133	9261	14399	1.02	0.0E+00	AW408788.1	EST_HUMAN	Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4134	9262	14400	1.94	0.0E+00	8922466	NT	U1-HF-BM0-adv-c-02-0-U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4134	9262	14401	1.94	0.0E+00	8922466	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4143	9271		2.37	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4155	9281	14417	0.99	0.0E+00	AB037739.1	NT	Homo sapiens mRNA for KIAA1318 protein, partial cds
4163	9289	14424	9.44	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element;

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4163	9289	14425	9.44	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_basalis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu
4167	9293	14431	1.19	0.0E+00	AF157476.1	NT	repetitive element; contains element MER35 repetitive element;
4181	9307	14444	1.22	0.0E+00	7662125	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4193	5216	10328	1.12	0.0E+00	AA228126.1	EST_HUMAN	Homo sapiens KIAA0440 protein (KIAA0440). mRNA
4193	5216	10328	1.12	0.0E+00	AA228126.1	EST_HUMAN	zr58c04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:687560 5' similar to TR:G2222811
4196	9321	14453	1.21	0.0E+00	7661969	NT	G2222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.
4199	9324	14464	13.69	0.0E+00	4758199	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
4199	9324	14455	13.69	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4208	9333		0.85	0.0E+00	AL163303.2	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4233	9358	14490	1.07	0.0E+00	AJ010770.1	NT	Homo sapiens chromosome 21 segment HS21C103
4247	9372	14505	4.01	0.0E+00	J02610.1	NT	Homo sapiens hyperion gene, exons 1-50
4282	9387	14524	1.06	0.0E+00	AW936689.1	EST_HUMAN	Human apolipoprotein B-100 mRNA, complete cds
4287	8475	13638	0.6	0.0E+00	BE779039.1	EST_HUMAN	PM2-DT0023-080300-004-q08 DT0023 Homo sapiens cDNA
4271	9395	14534	4.79	0.0E+00	AF174590.1	NT	60146495F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3688246 5'
4279	9402	14541	0.64	0.0E+00	6806918	NT	Homo sapiens F-box protein Fbx4 (FBL4) mRNA, partial cds
4279	9402	14542	0.64	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4280	9403		2.49	0.0E+00	AI189844.1	EST_HUMAN	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4284	9406		4.17	0.0E+00	U14520.1	NT	q23f06.x1 Soares_placenta_86c9weeks_2NbHP6c9W Homo sapiens cDNA clone IMAGE:1724579 3'
4287	9409	14545	1.04	0.0E+00	5174574	NT	similar to contains MER20.b2 MER20 repetitive element;
4298	9418	14551	0.91	0.0E+00	4505846	NT	Human GBFA3 (Chia3) gene, partial cds
4302	9424	14558	1.01	0.0E+00	6563384	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) leukemia) (t(11q24)) mRNA
4302	9424	14559	1.01	0.0E+00	6563384	NT	Homo sapiens protein convertase subtilisin/kexin type 2 (PCSK2) mRNA
4308	9430	14565	1.11	0.0E+00	U10991.1	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4308	9430	14566	1.11	0.0E+00	U10991.1	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4318	9440	14573	8.66	0.0E+00	6912281	NT	Human G2 protein mRNA, partial cds
4338	9460		1.1	0.0E+00	AF153047.2	NT	Homo sapiens G2 protein mRNA, partial cds
4343	9465	14601	1.31	0.0E+00	U03901.1	NT	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds
4349	9471	14608	4.62	0.0E+00	L14561.1	NT	Human Ig light chain VL1 region germline (hum1c2c) gene, partial cds
							Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds

Page 209 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4353	9475	14613	4.82	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
4353	9475	14614	4.82	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
4354	9476	14615	1.17	0.0E+00	AW166933.1	EST_HUMAN	cg88e10.x1 NCI_CGAP U14 Homo sapiens cDNA clone IMAGE:2633514 3' similar to TR:P67365 P67365
4360	9482	14621	1.55	0.0E+00	X60483.1	NT	ZINC FINGER PROTEIN 64;
4360	9482	14622	1.55	0.0E+00	X60483.1	NT	H.sapiens H4/d gene for H4 histone
4365	9486	14628	8.91	0.0E+00	7662091	NT	H.sapiens H4/d gene for H4 histone
4365	9486	14628	8.91	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4365	9486	14629	8.91	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4373	9494	14638	1.28	0.0E+00	X82338.1	NT	Homo sapiens Menkes disease gene, exon 4
4376	9497	14642	15.1	0.0E+00	4886126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4377	9498	14643	1.48	0.0E+00	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4378	9499	14645	0.98	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4381	9502	14645	1.08	0.0E+00	AB037781.1	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4410	9530	14670	1.24	0.0E+00	7019453	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4420	9540	14684	6.61	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4426	9546	14684	2.27	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4426	9546	14685	2.27	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4430	9549	14691	0.75	0.0E+00	W26179.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4430	9549	14692	0.75	0.0E+00	W26179.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4447	9566	14692	2.08	0.0E+00	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
4467	9586	14723	1	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
4478	9598	14737	31.08	0.0E+00	AW084984.1	EST_HUMAN	xc68e08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW:AHNK_HUMAN
4480	10310	14737	1.72	0.0E+00	8051619	NT	Q09666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK ;
4482	9601	14740	0.91	0.0E+00	AF016050.1	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4484	9603	14749	8.23	0.0E+00	AL163207.2	NT	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds
4491	9610	14749	1.27	0.0E+00	AJ278120.1	NT	Homo sapiens chromosome 21 segment HS21C007
4491	9610	14750	1.27	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4493	9612	14752	1.18	0.0E+00	4768467	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4494	9613	14753	2.95	0.0E+00	AF108930.1	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4499	9618	14759	1.01	0.0E+00	4506962	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
4504	9623	14765	1.14	0.0E+00	S76684.1	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylneuraminase: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8) mRNA
4504	9623	14765	1.14	0.0E+00	S76684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon

Page 210 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4505	9624	14786	1.38	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4506	9624	14787	1.38	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4512	10311	14775	2.71	0.0E+00	6008973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4517	9635	14780	5.93	0.0E+00	AF208101.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4522	9840	14787	1.15	0.0E+00	AF152337.1	NT	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4525	9843	14791	1.96	0.0E+00	5454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4536	9654	14799	44.34	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4543	9661	14804	0.97	0.0E+00	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4547	9665	14807	1.06	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4552	9670	14813	1.48	0.0E+00	4502556	NT	Homo sapiens calcitriol/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4555	9673		1.52	0.0E+00	BE871908.1	EST_HUMAN	601447832F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3862127 5'
4558	9678		2.62	0.0E+00	L35485.1	NT	Homo sapiens iduronate sulphate sulphasase (IDS) gene, complete cds
4560	9678	14816	10.58	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4560	9678	14817	10.58	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4575	9693	14830	2.49	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
						NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4578	9696	14833	10.97	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4578	9696	14834	10.97	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4593	9711		2.31	0.0E+00	AA174072.1	EST_HUMAN	zp18g08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4595	9713		1.47	0.0E+00	7657410	NT	Homo sapiens cdz (odd Ozfien-m, Drosophila) homolog 1 (ODZ1), mRNA
4597	9715		2.4	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4598	9716	14852	1.36	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4598	9717	14853	4.87	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4600	9718		1.71	0.0E+00	AB037521.1	NT	Homo sapiens gene for reticulic protein, partial cds
4602	9720	14854	0.74	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4606	9724	14859	0.98	0.0E+00	AB007886.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4609	9727	14863	1.09	0.0E+00	AL162331.1	NT	Novel human gene mapping to chromosome 1
4611	9729	14866	30.74	0.0E+00	4667887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4611	9729	14868	30.74	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4612	9730	14867	2.56	0.0E+00	AF187441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4621	9739	14878	0.91	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4621	9739	14879	0.91	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds



Page 211 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4621	9739	14880	0.91	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4622	9740	14881	1.18	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4622	9740	14882	1.18	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4629	9747	14892	10.76	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4635	9753	14900	1.28	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-105 BT0635 Homo sapiens cDNA
4636	9754	14901	1.42	0.0E+00	AA418246.1	EST_HUMAN	z96807.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:767605 3'
4843	9781		2.12	0.0E+00	AF089941.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4850	9787	14912	2.23	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4850	9787	14913	2.23	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4851	9788	14914	2.34	0.0E+00	M74099.1	NT	Human displacement protein (OCAAT) mRNA
4854	9771	14917	1.02	0.0E+00	AW294800.1	EST_HUMAN	UI-H-B12-ah1-c-05-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726792 3'
4854	9771	14918	1.02	0.0E+00	AW294800.1	EST_HUMAN	UI-H-B12-ah1-c-05-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726792 3'
4856	9773	14919	2.18	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4856	9773	14920	2.18	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4858	5332	10477	4.19	0.0E+00	T6945.1	EST_HUMAN	ye83g04.12 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4858	5332	10478	4.19	0.0E+00	T6945.1	EST_HUMAN	ye83g04.12 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4881	9797	14942	44.66	0.0E+00	M80902.1	NT	Human AHNK nucleoprotein mRNA, 5' end
4884	9800	14945	1.91	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4884	9800	14946	1.91	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4888	9804	14951	1.82	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTTR) gene, complete cds
4889	9805	14952	0.73	0.0E+00	7662479	NT	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
4891	9807	14953	2.53	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4897	9813	14961	1.66	0.0E+00	U07593.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds
4702	9818	14966	1.18	0.0E+00	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4709	9826		1.28	0.0E+00	X58467.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D6
4715	9831	14973	1.09	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4715	9831	14974	1.09	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4725	9838	14982	1.27	0.0E+00	AF028801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-28
4727	9840	14984	1.04	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4727	9840	14985	1.04	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4729	9842	14987	0.83	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (AD013), mRNA
4729	9842	14988	0.83	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (AD013), mRNA

Page 212 of 214  
Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4753	9866	15015	1.74	0.0E+00	AW444637.1	EST_HUMAN	U1-H-B13-gjw-c-04-0-UI.s1 NC1 CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733284 3'
4759	9872	15023	1.41	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4762	9876		1.63	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-Iso mRNA, complete cds
4807	9919	15060	1.09	0.0E+00	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1) mRNA
4810	9922						Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4814	9926	15067	4.79	0.0E+00	AF240786.1	NT	M fascicularis mRNA for metalloproteinase-like, disintegrin-like protein, IVa
4816	9928	15069	3.29	0.0E+00	X87205.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSOR9) mRNA, complete cds
4818	9930	15071	2.79	0.0E+00	AF084479.1	NT	Mus musculus zinc finger transcription factor Kalso mRNA, complete cds
4819	9931	15072	2.11	0.0E+00	AF097416.1	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4821	9933	15074	4.47	0.0E+00	4503766	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC) mRNA
4822	9934	15075	27.4	0.0E+00	4885048	NT	ZINC FINGER PROTEIN 132
4824	9936	15077	1.43	0.0E+00	P52740	SWISSPROT	Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312) mRNA
4827	9939	15081	1.33	0.0E+00	8922180	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073) mRNA
4831	9943	15085	8.77	0.0E+00	8923080	NT	Homo sapiens KIAA0187 gene product (KIAA0187) mRNA
4832	9944	15086	1.25	0.0E+00	7681979	NT	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tor-alpha) gene, J1-J61 segments; and Tor-C-alpha gene, exons 1-4
4832	9944	15086	1.61	0.0E+00	M94081.1	NT	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tor-alpha) gene, J1-J61 segments; and Tor-C-alpha gene, exons 1-4
4834	9946	15089	1.61	0.0E+00	M94081.1	NT	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tor-alpha) gene, J1-J61 segments; and Tor-C-alpha gene, exons 1-4
4834	9946	15089	1.15	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4834	9946	15089	1.15	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4838	9950	15094	2.24	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4840	9952	15097	2.24	0.0E+00	7706604	NT	Homo sapiens MAGC-C2 (MAGC2) mRNA
4848	9960	15104	1.05	0.0E+00			Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF21) mRNA
4854	9966	15111	1.26	0.0E+00	5032150	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2) mRNA
4856	9968	15113	0.6	0.0E+00	6806918	NT	H. sapiens MICA gene
4858	9970	15115	1.3	0.0E+00	X82841.1	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4859	9971	15116	2.22	0.0E+00	4586642	NT	Homo sapiens mRNA for KIAA1443 protein, partial cds
4860	9972	15117	1.28	0.0E+00	AB037864.1	NT	H. sapiens fertilin alpha pseudogene
4861	9973	15118	0.9	0.0E+00	Y09232.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4862	9974	15119	2.01	0.0E+00	AB014533.1	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1) mRNA
4863	9975	15120	2.39	0.0E+00	6677648	NT	Homo sapiens meningioma expressed antigen 8 (colled-coil proline-rich) (MGEA8) mRNA
4864	9976	15121	1.5	0.0E+00	5174590	NT	QV6-BN0147-280400-213-g11 BN0147 Homo sapiens cDNA
			2.16	0.0E+00	BE007935.1	EST_HUMAN	

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4884	9976	15122	2.16	0.0E+00	BE007935.1	EST_HUMAN	QVQ-BN0147-280400-213-g11 BN0147 Homo sapiens cDNA
4886	9978	15124	10.15	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4867	9979	15125	1.35	0.0E+00	Y16723.1	NT	Homo sapiens gene encoding filensin, exon 8
4868	9980	15126	1.63	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
4868	9980	15126	1.63	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
4868	9980	15127	1.63	0.0E+00	5174560	NT	Homo sapiens zinc-finger DNA-binding protein (HUMHOX1), mRNA
4869	9981	15128	1.42	0.0E+00	7705546	NT	Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RHD, therad 7
4870	9982		3.34	0.0E+00	AJ010442.1	NT	Homo sapiens MHC class 1 region
4873	9984	15131	6.4	0.0E+00	AF055086.1	NT	Homo sapiens opicoid receptor, delta 1 (OPRD1) mRNA
4875	9986		2.08	0.0E+00	4505508	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4876	9987	15134	2.43	0.0E+00	AF091711.1	NT	Homo sapiens partial TTN gene for titin
4880	9991	15138	1.15	0.0E+00	AJ277892.1	NT	Homo sapiens COL4A6 gene for $\alpha 6(V)$ collagen, exon 44 and partial cds
4890	10001	15147	0.95	0.0E+00	D63562.1	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPS) mRNA
4894	10005	15149	1.58	0.0E+00	4503684	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylneuraminato: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8) mRNA
4902	9918	14789	0.97	0.0E+00	4506952	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4914	10024	15168	1.18	0.0E+00	AB028898.1	NT	Homo sapiens chromosome 21 segment HS21C084
4932	10042	15182	1.47	0.0E+00	AL163284.2	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
4938	10048	15186	0.81	0.0E+00	7682318	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
4946	10055	15193	0.7	0.0E+00	AA205437.1	EST_HUMAN	z466b06.e1 Stragene neuroepithelium (J937231) Homo sapiens cDNA clone IMAGE:646547 3'
4950	10059	15197	1.45	0.0E+00	8922926	NT	Homo sapiens hypothetical protein FLJ11190 (FLJ11190), mRNA
4951	9998	15144	0.93	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4953	10061	15200	0.97	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
4957	10065		5.03	0.0E+00	U14987.1	NT	Human ribosomal protein L21 mRNA, complete cds
4967	10075	15213	1.86	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
4969	10077		2.72	0.0E+00	BE408863.1	EST_HUMAN	607303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'
4973	10081	15218	6.21	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4981	10089	15222	1.12	0.0E+00	AB028566.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
4995	10101	15231	2.04	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
4995	10101	15232	2.04	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5007	10111	15240	0.78	0.0E+00	AA601246.1	EST_HUMAN	h014g09.s1 NCL_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5007	10111	15241	0.78	0.0E+00	AA801246.1	EST_HUMAN	nt14g09.s1 NCJ CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704.3 similar to TR:E239140
5007	10111	15242	0.78	0.0E+00	AA601246.1	EST_HUMAN	E239140 SPALT PROTEIN;
5016	5403	10547	0.87	0.0E+00	AF196658.1	NT	nt14g09.s1 NCJ CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704.3 similar to TR:E239140
5018	10120		0.94	0.0E+00	4758225	NT	E239140 SPALT PROTEIN;
5028	10130	15259	1.39	0.0E+00	AF018705.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5036	10138		1.19	0.0E+00	AL183209.2	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5039	10141		44.4	0.0E+00	D50657.1	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5089	10171	15306	3.62	0.0E+00	X52988.1	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5070	10172	15307	0.72	0.0E+00	X72791.1	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5102	10203	15342	1.17	0.0E+00	4567362	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5104	10205	15343	0.76	0.0E+00	5902055	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5108	10209	15346	1.05	0.0E+00	Y08032.1	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5120	10221	15355	0.62	0.0E+00	5902091	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5121	10222	15356	1.03	0.0E+00	AF124250.1	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5136	10236	15372	1.31	0.0E+00	7682421	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5142	10242	15378	0.95	0.0E+00	AF108830.1	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5142	10242	15379	0.95	0.0E+00	AF108830.1	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5143	10243	15380	0.91	0.0E+00	U71601.1	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5146	10246	15384	1.01	0.0E+00	4757889	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5147	10247	15385	0.98	0.0E+00	AF195668.1	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5151	10251	15390	0.95	0.0E+00	4826777	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5160	10260		0.94	0.0E+00	AB040948.1	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5179	10276	15414	1.32	0.0E+00	BE144725.1	EST_HUMAN	OM0-H10178-051099-084-e05 H10178 Homo sapiens cDNA

## CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived  
5 from human Breast comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 5,205 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid  
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid  
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 5,206 - 10,317.
5. A spatially-addressable set of single exon nucleic acid  
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid  
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid  
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid  
5 probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid  
10 probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid  
15 probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid  
20 probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of  
25 single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human  
gene expression in a sample derived from human Breast  
30 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 5,205 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human Breast.

35

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 5,206 - 10,317 or a complementary sequence or a fragment thereof.
- 5
15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of  
10 SEQ ID NOs.: 10,318 - 15,438, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Breast.
16. A single exon nucleic acid probe as claimed in any one  
15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
17. A single exon nucleic acid probe as claimed in any one  
20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.
18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.
- 25
19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.
- 30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
21. A single exon nucleic acid probe as claimed in any one  
35 of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human Breast, comprising:

5       contacting the microarray of claim 12, with a first  
          collection of detectably labeled nucleic acids,  
          said first collection of nucleic acids derived  
          from mRNA of human Breast; and then  
          measuring the label detectably bound to each probe of  
10       said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

          algorithmically predicting at least one exon from  
15       genomic sequence of said eukaryote; and then  
          detecting specific hybridization of detectably labeled  
          nucleic acids to a single exon probe,  
          wherein said detectably labeled nucleic acids are derived  
          from mRNA from the Breast of said eukaryote, said probe is  
20       a single exon probe having a fragment identical in sequence  
          to, or complementary in sequence to, said predicted exon,  
          said probe is included within a microarray according to  
          claim 12, and said fragment is selectively hybridizable at  
          high stringency.

25

24. A method of assigning exons to a single gene, comprising:

          identifying a plurality of exons from genomic  
          sequence according to the method of claim 23; and  
30       then  
          measuring the expression of each of said exons in a  
          plurality of tissues and/or cell types using  
          hybridization to single exon microarrays having a  
          probe with said exon,  
35       wherein a common pattern of expression of said exons in



said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID  
5 NOS: 1 - 10,317 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of  
SEQ ID Nos: 1 - 10,317.

10 27. A peptide comprising a sequence as set out in any of  
SEQ ID Nos: 10,318 - 15,438.

1/10

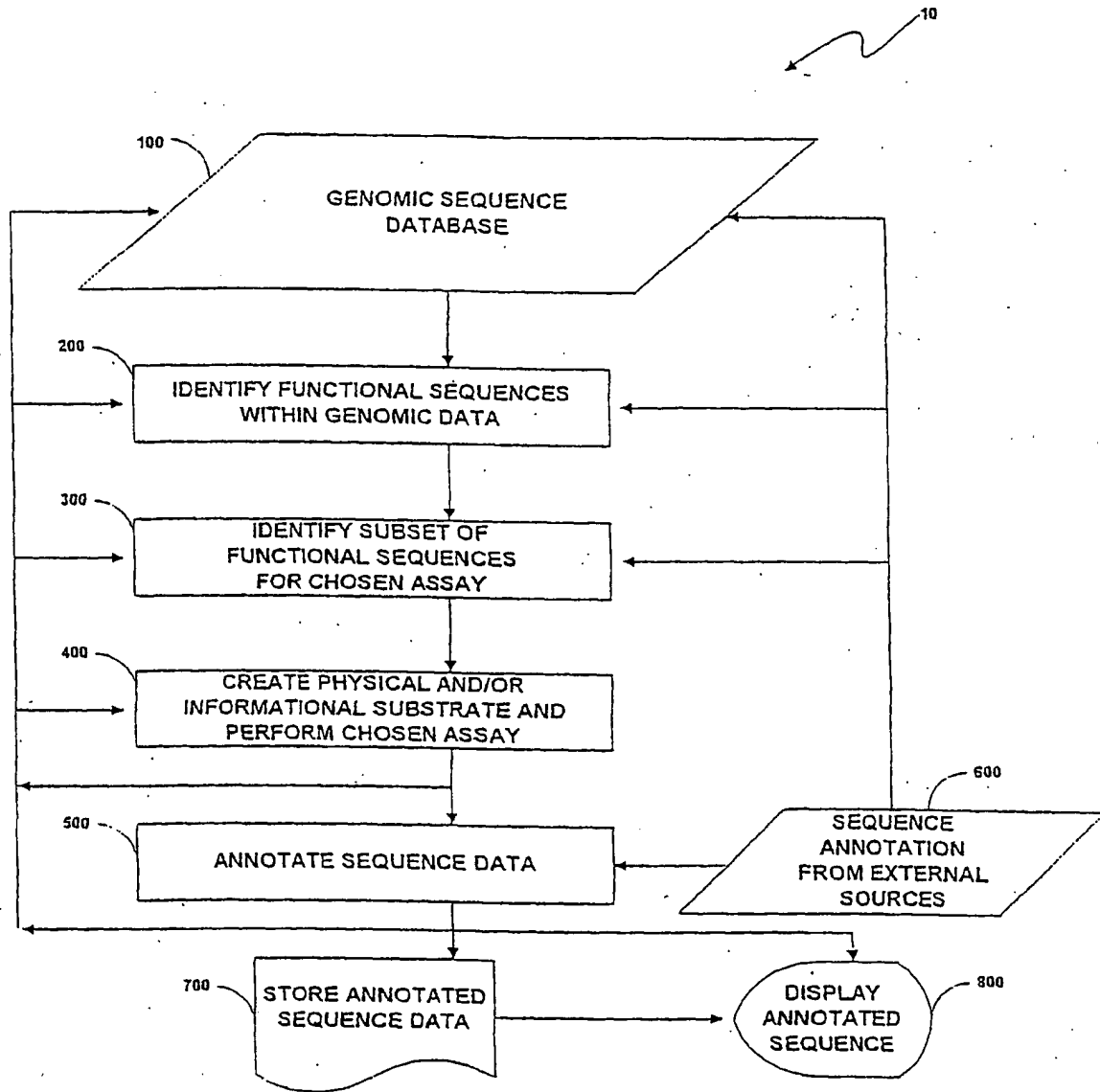


Fig. 1

2/10

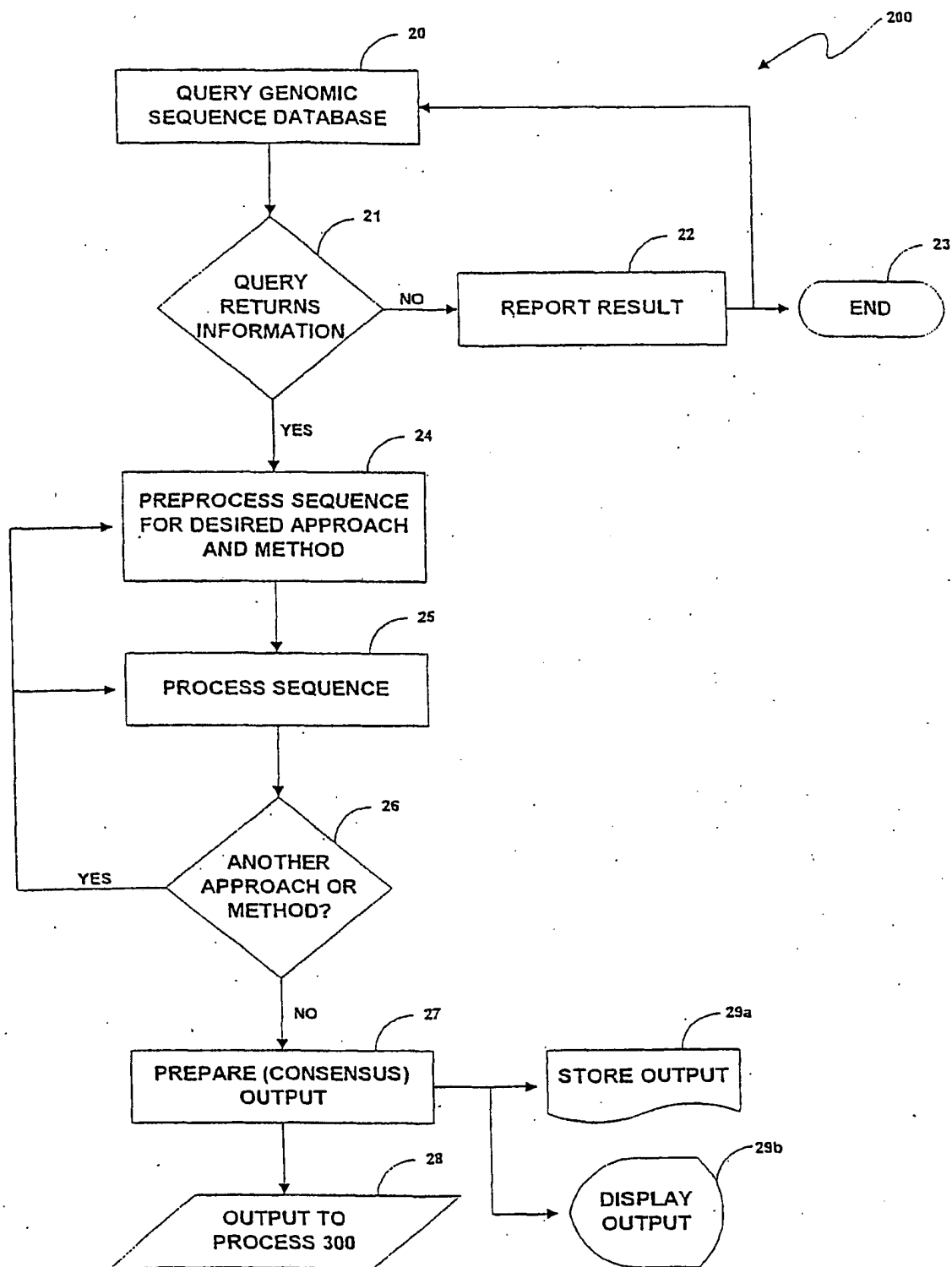


Fig. 2

3/10

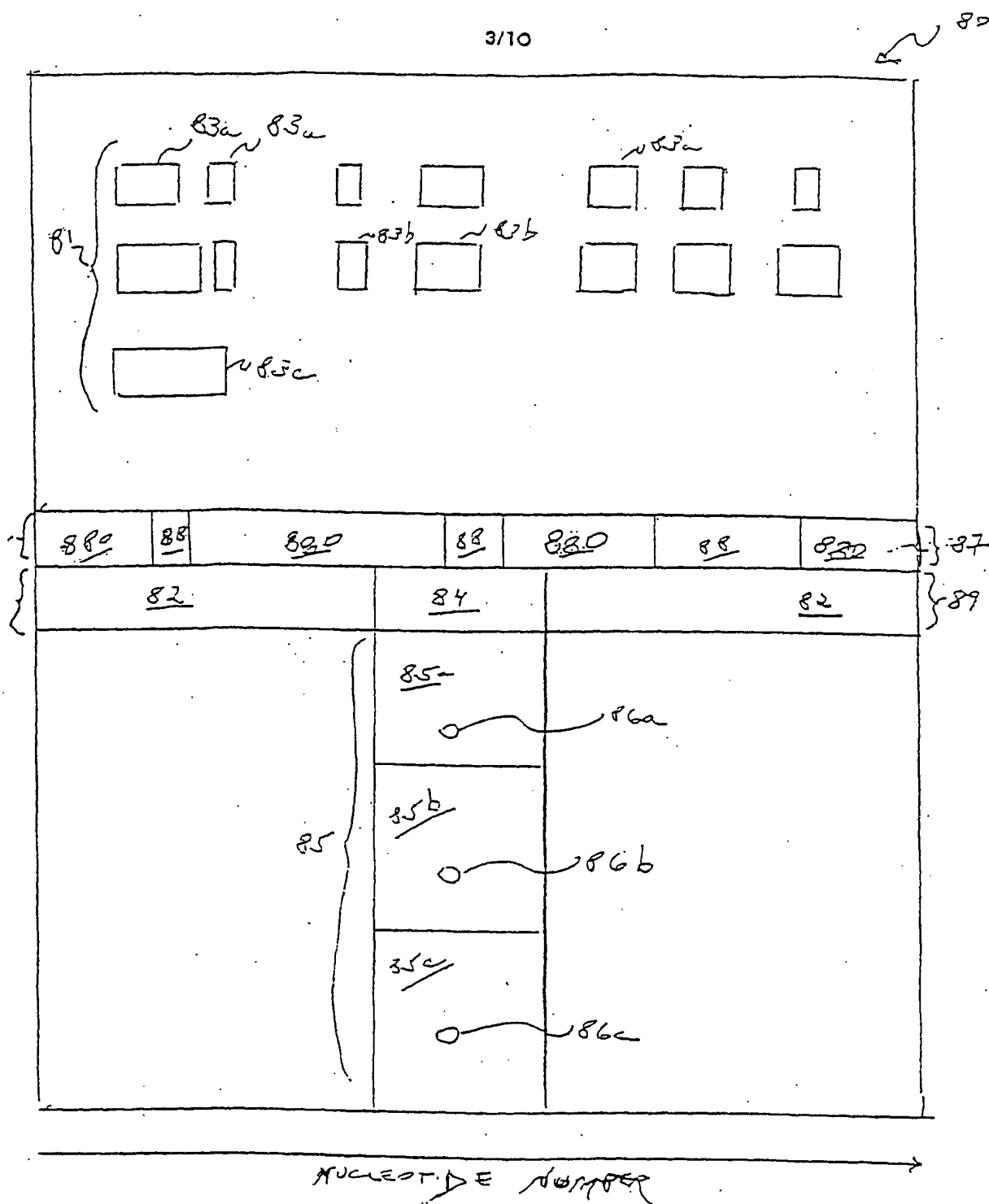


Fig. 3

4/10

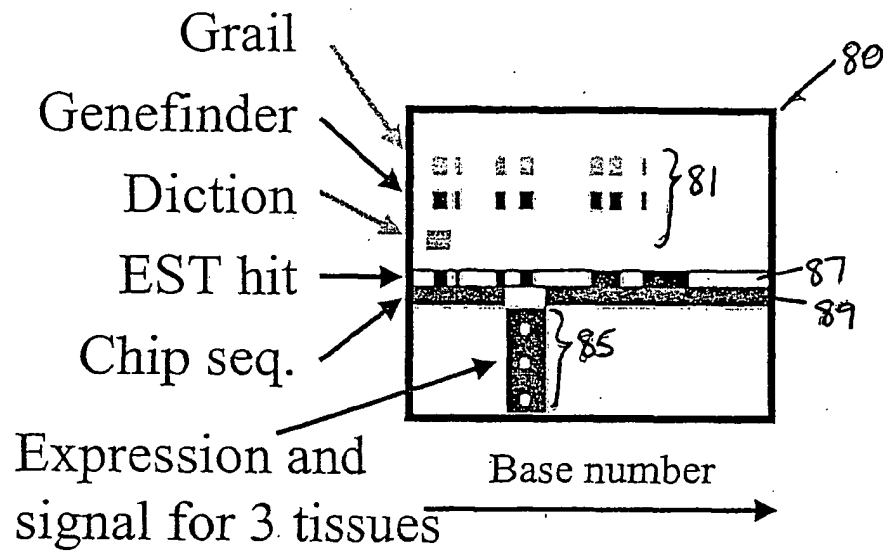


Fig. 4

5/10

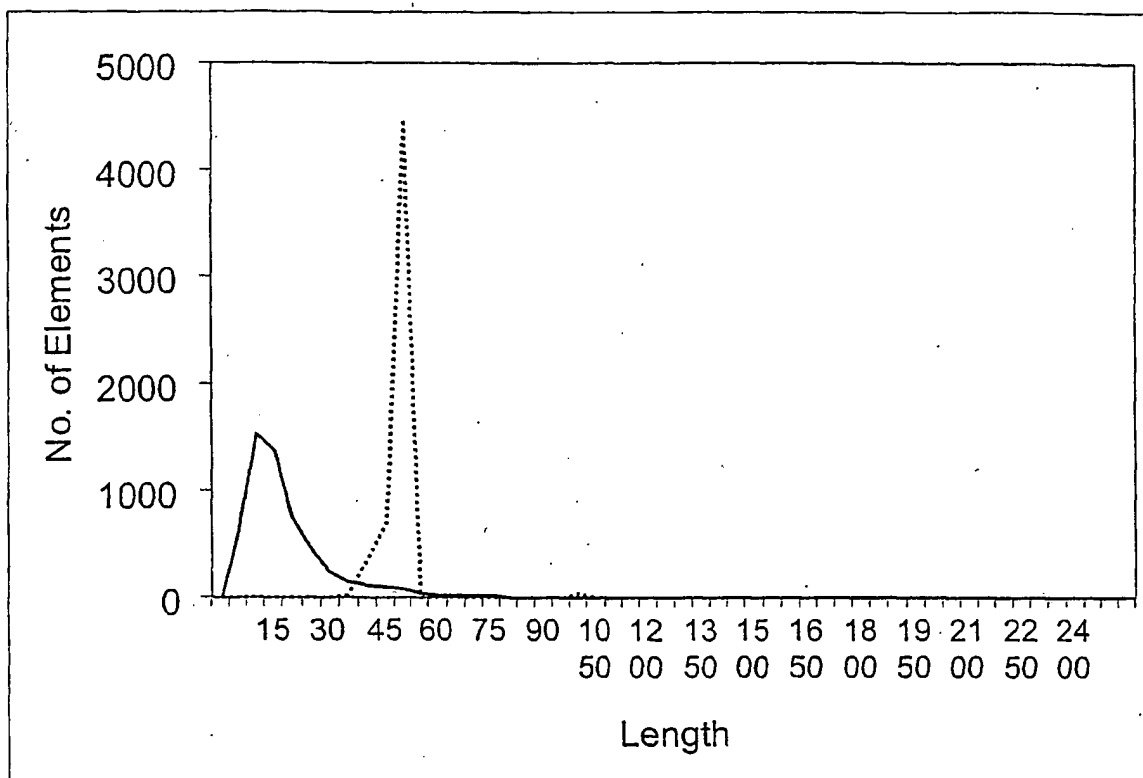


Fig. 5

6/10

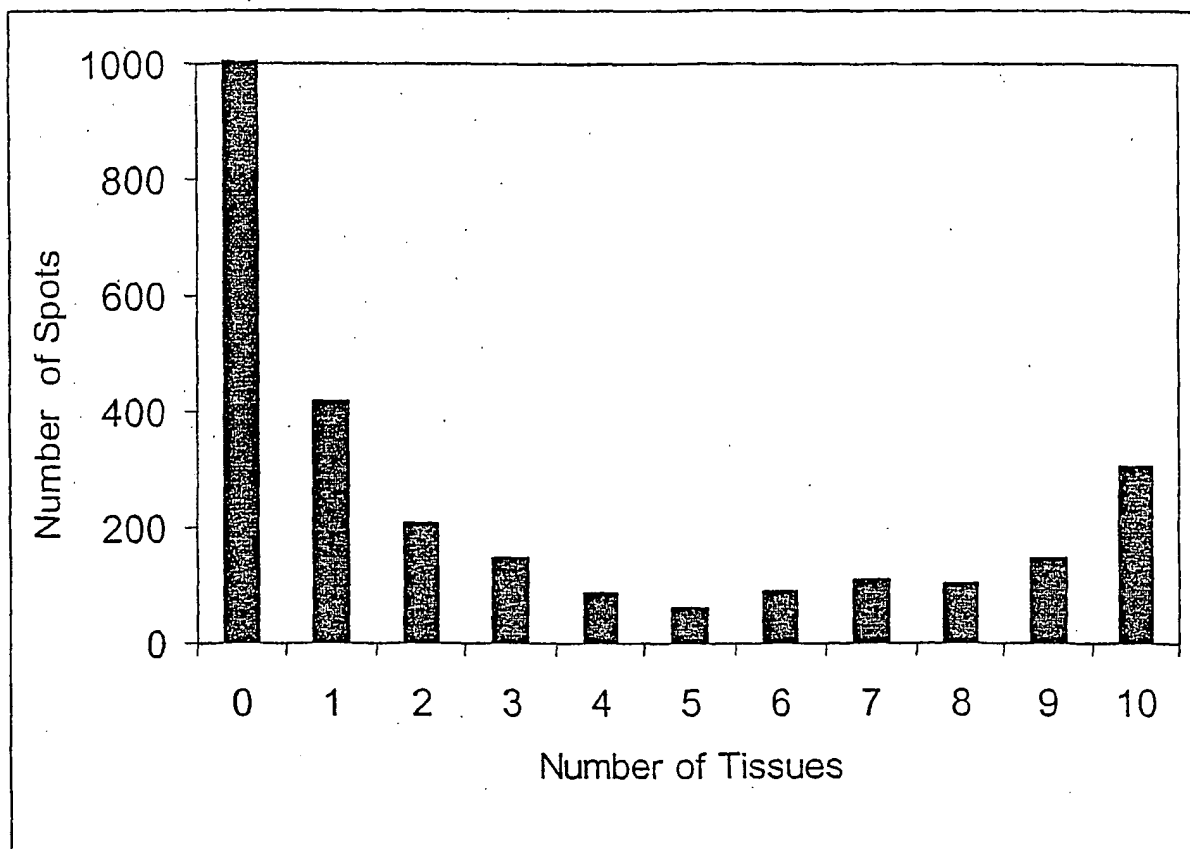


Fig. 6

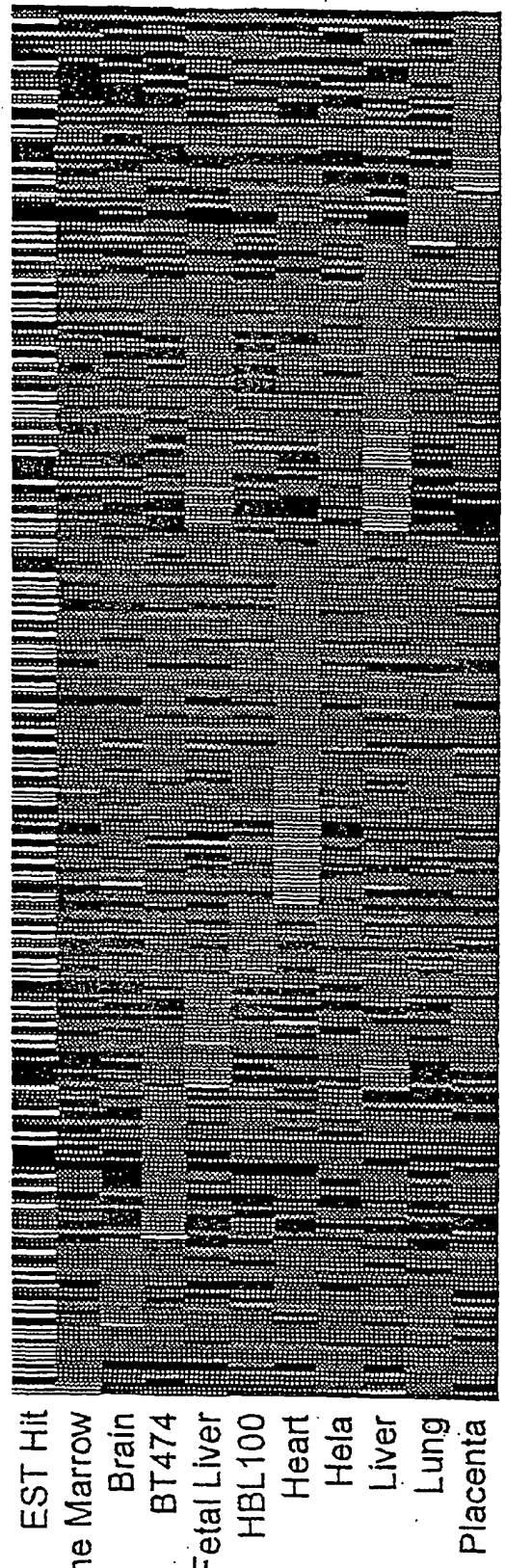


Fig. 7a

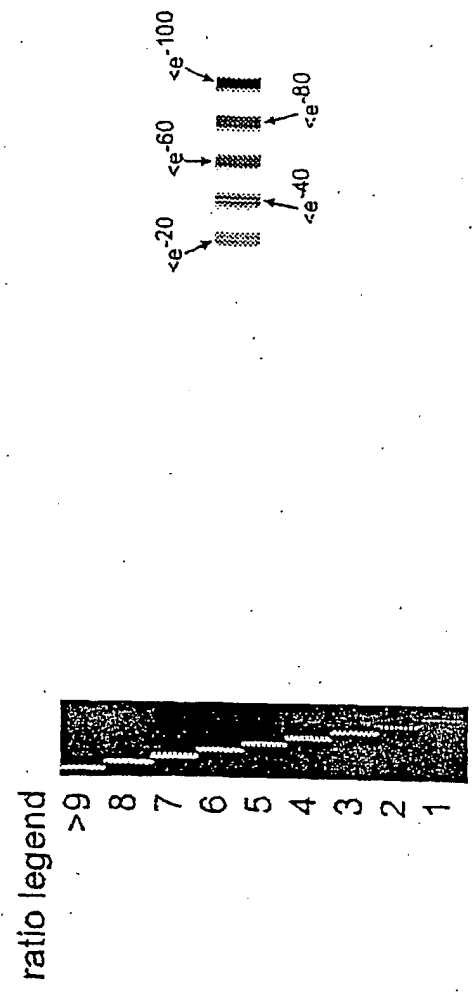


Fig. 7b

Fig. 7c



8/10

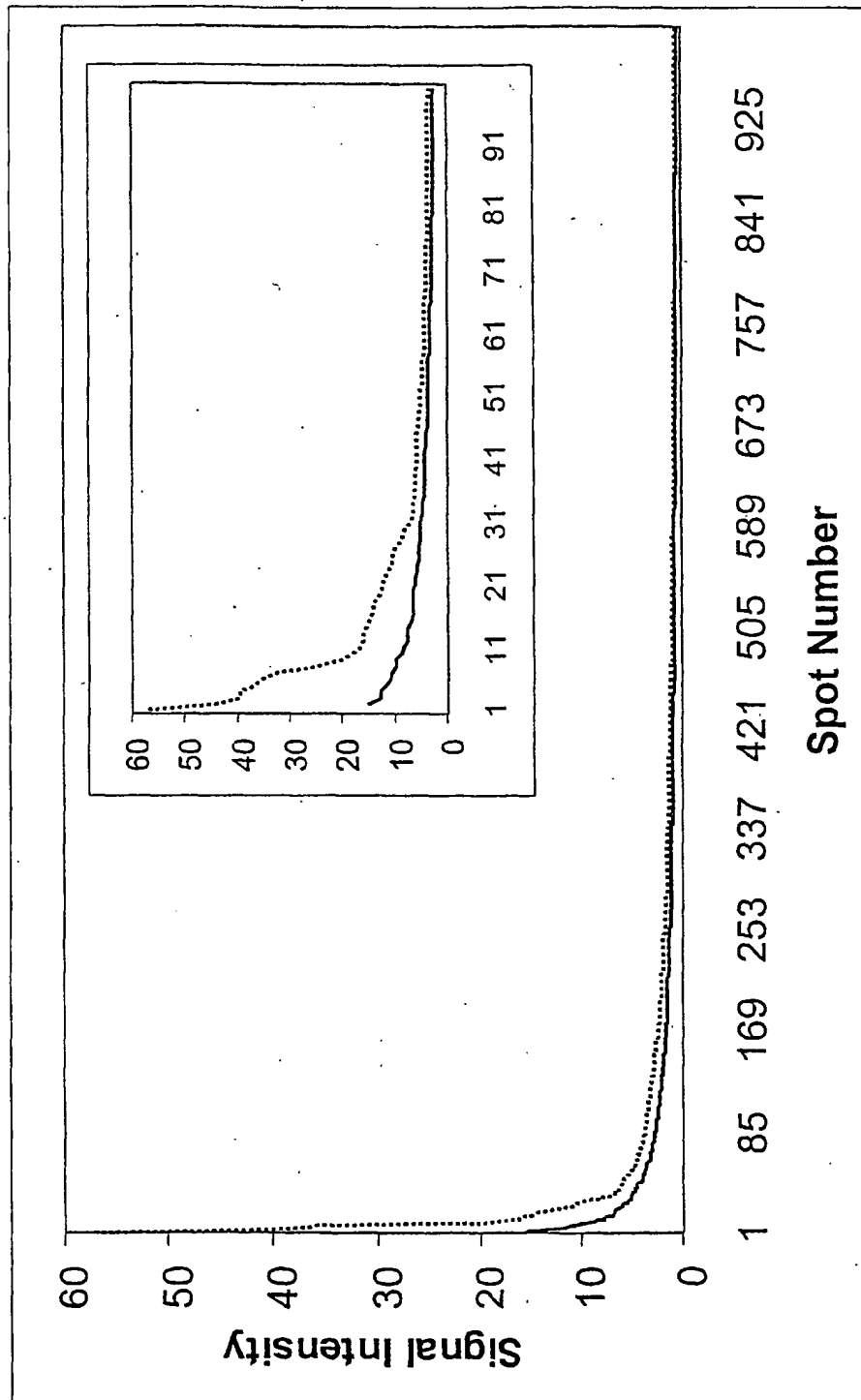


Fig. 8

9/10

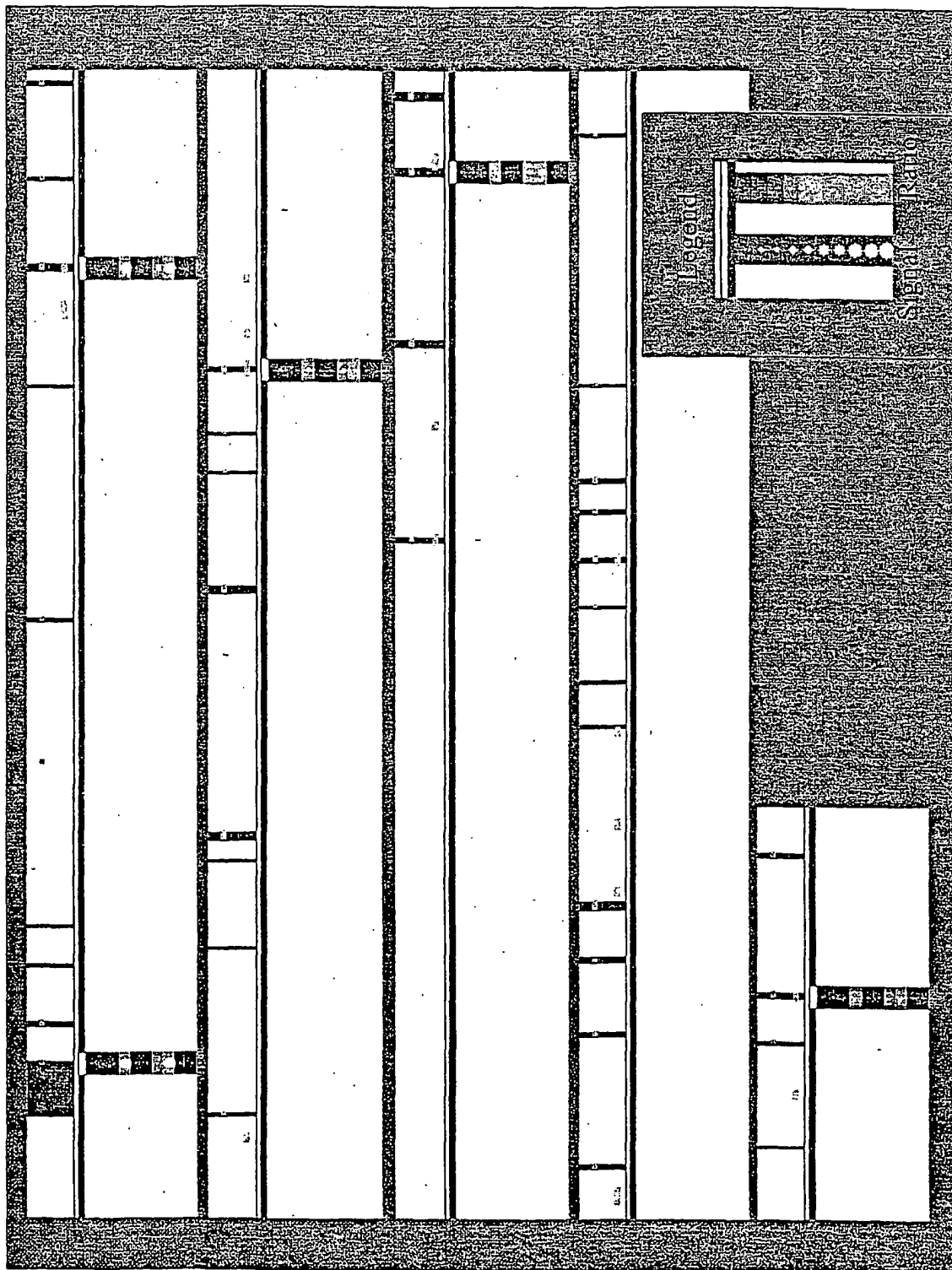
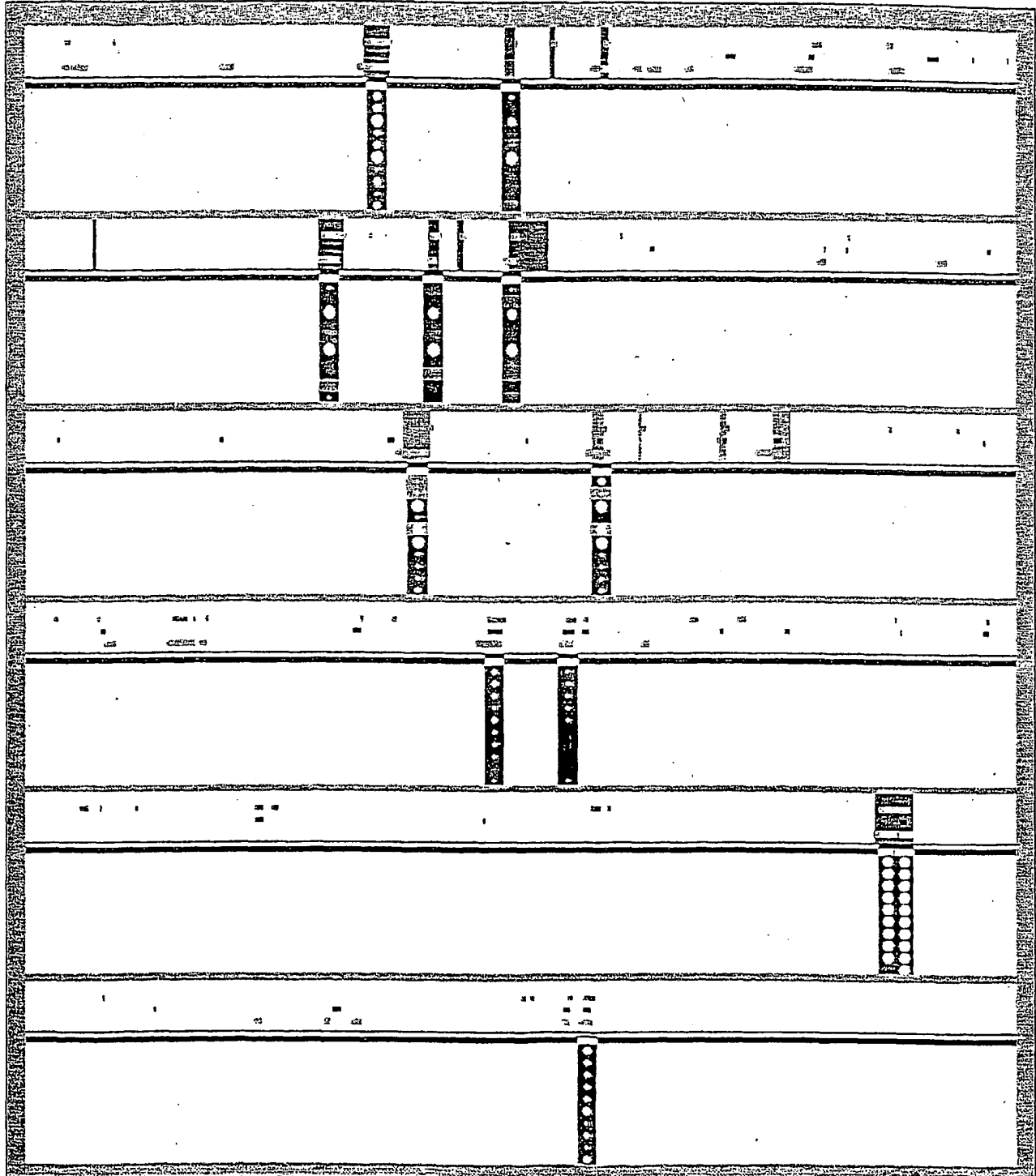


Fig. 9

10/10

Fig. 10



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09/632,366	3 August 2000 (03.08.2000)	US
60/234,687	21 September 2000 (21.09.2000)	US
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(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND BT 474 CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human BT 474 cells is described. Also described are single exon nucleic acid probes expressed in the BT 474 cells and their use in methods for detecting gene expression.

WO 01/057271 A3

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00662

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C1201/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, CHEM ABS Data, EMBASE, SCISEARCH, MEDLINE, EMBL

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL 'Online! 11 May 1999 (1999-05-11) HEILIG ET AL.: "Sequencing of the human chromosome 14" Database accession no. AL049837 XP002182997	13-21, 25
Y	abstract	1-12, 22-24, 26, 27

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

## \* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&amp;" document member of the same patent family

Date of the actual completion of the international search

12 July 2002

Date of mailing of the international search report

07.08.2002

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Bort, S

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00662

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL 'Online! 14 November 1997 (1997-11-14) ADAMS ET AL.: "Use of a random BAC End sequence database for sequence-ready map building" Database accession no. B57793 XP002186124</p>	13-21,25
Y	abstract	1-12, 22-24, 26,27
X	<p>--- DATABASE EMBL 'Online! 9 May 1997 (1997-05-09) MARRA ET AL.: "The WashU-HHMI Mouse EST Project" Database accession no. AA414703 XP002205620</p>	13-21,25
Y	abstract	1-12, 22-24, 26,27
X	<p>--- DATABASE SWALL 'Online! 1 July 1997 (1997-07-01) "pro-pol-dutpase polyprotein (fragment)" Database accession no. 002711 XP002037954 abstract &amp; BENIT ET AL.: "Cloning of a new murine endogenous retrovirus, MuERV-L, with strong similarity to the human HERV-L element with a gag coding sequence closely related to the Fv1 restriction gene" J. VIROL., vol. 71, 1997, page 5652</p>	26,27
Y	<p>WO 98 30722 A (MACK DAVID H) 16 July 1998 (1998-07-16) the whole document</p>	1-12, 22-24
Y	<p>--- BURGE C ET AL: "Prediction of complete gene structure in human genomic DNA" JOURNAL OF MOLECULAR BIOLOGY, LONDON, GB, vol. 268, no. 1, 25 April 1997 (1997-04-25), pages 78-94, XP002109301 ISSN: 0022-2836 the whole document</p>	1-12, 22-24, 26,27
Y	<p>--- CHURCH D M ET AL: "ISOLATION OF GENES FROM COMPLEX SOURCES OF MAMMALIAN GENOMIC DNA USING EXON AMPLIFICATION" NATURE GENETICS, NEW YORK, NY, US, vol. 6, 1994, pages 98-105, XP000608940 ISSN: 1061-4036 the whole document</p>	1-12, 22-24, 26,27
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	-/--	

# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 01/00662

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>LIPSHUTZ R J ET AL: "High density synthetic oligonucleotide arrays." NATURE GENETICS, (1999 JAN) 21 (1 SUPPL) 20-4. REF: 32 , XP002182912 the whole document</p> <p>-----</p>	1-12

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 01/00662

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:  
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:  
1-27 (all partially)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.



## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

## Continuation of Box I.2

The following statements about the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject matter for which a search has been performed and identified as the first and second inventions in form 206 PCT.

Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising Seq. Id 1 or 2, as well as microarrays comprising said sets. In fact, the claims contain so many possible permutations, that a lack of conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search for the sets of probes comprising Seq. Id 1 or 2 has been limited to the Seq. Id as such.

Claims 1-3, 5, 6, 8-15 and 18-24 relate to portions or fragments of nucleic acids defined by Seq. Id. 1 or 2. The length or other similar characterizing features of the portions or fragments is not disclosed, bringing the total number of possible prior art sequences to exceptionally high numbers. The shorter the length, the higher the possibility that an overflow of, in principle unrelated, sequences are retrieved, making the establishment of a meaningful International Search Report impossible. For this reason the search has been limited to portions or fragments of Seq. Id. 1 or 2 having a significant minimum length and being supported by the description, namely at least 15 contiguous nucleotides (see claim 16).

Claims 15-21 relate to an extremely large number of nucleic acid probes. The probes are defined solely by their potential to code for peptide Seq. Id. 10326. However, due to the degeneracy of the genetic code, every peptide is potentially coded by an extremely high number of nucleic acid sequences. In fact, the claims contain so many potential nucleic acid sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole of the claimed scope impossible. The search has therefore been carried out for those parts of the claim which do appear to be clear and concise, namely the nucleic acid sequences disclosed in the application and identified as encoding the referred peptide in table 4 (Seq. Ids. 1 or 2 and 5214).

Likewise, claim 26, which refers to peptides encoded by Seq. Id. 1 or 2 and 5214, encompasses a high and undefined number of possible peptides. Besides three possible reading frames deriving from the encoding nucleic acid strand, as well as three additional reading frames deriving from the complementary nucleic acid strand, every possible fragment of these is being covered by the claim. This is due to the potential presence of stop codons within any of the six possible reading frames which can not be established a priori. Thus, claim 26 contains so many potential peptide sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search has been carried out for those parts of the claim which do appear to be

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

clear and concise, namely the peptide disclosed, identified by Seq. Id. 10326.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-27 (all partially)

A nucleic acid probe comprising SEQ ID 1, complementary sequences or fragments thereof (in particular comprising SEQ ID 5214). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by SEQ ID 1 (in particular the one defined by SEQ ID 10326).

Invention 2: claims 1-27 (all partially)

A nucleic acid probe comprising SEQ ID 2, complementary sequences or fragments thereof (in particular comprising SEQ ID 5214). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by SEQ ID 2 (in particular the one defined by SEQ ID 10326).

Inventions 3-5205: claims 1-27 (all partially)

A nucleic acid probe comprising SEQ ID n (where n ranges from 3-5205 according to the invention number above), complementary sequences or fragments thereof, in particular comprising the SEQ ID no. which is listed in the column "Exon SEQ ID no." in the same row that contains SEQ ID n in table 4. Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by SEQ ID n, in particular the one defined by the SEQ ID no in the column "ORF SEQ ID no" of the same row where SEQ ID n is listed.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 01/00662

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9830722	A	16-07-1998	AU 6035698 A	03-08-1998
			EP 0973939 A1	26-01-2000
			JP 2001508303 T	26-06-2001
			US 6303301 B1	16-10-2001
			WO 9830722 A1	16-07-1998
			US 2002028454 A1	07-03-2002
			US 2002039739 A1	04-04-2002

CORRECTED VERSION

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International Bureau(43) International Publication Date  
9 August 2001 (09.08.2001)(10) International Publication Number  
PCT WO 01/57271 A2

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| 60/207,456 | 26 May 2000 (26.05.2000)       | US |
| 09/608,408 | 30 June 2000 (30.06.2000)      | US |
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| 60/236,359 | 27 September 2000 (27.09.2000) | US |
| 0024263.6  | 4 October 2000 (04.10.2000)    | GB |
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- Published:**
- without international search report and to be republished upon receipt of that report
  - with sequence listing part of description published separately in electronic form and available upon request from the International Bureau
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- (48) Date of publication of this corrected version: 6 December 2001
- (72) Inventors; and
- (75) Inventors/Applicants (*for US only*): PENN, Sharron, G. [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). HANZEL, David, K. [US/US]; 988 Loma Verde Avenue, Palo Alto, CA 94303 (US). CHEN, Wensheng [CN/US]; 210 Easy Street, #25, Mountain View, CA 94043 (US). RANK, David, R. [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).
- (15) Information about Correction: see PCT Gazette No. 49/2001 of 6 December 2001, Section II
- (74) Agent: RONNING, Royal, N., Jr.: Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ 08855 (US).
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND BT 474 CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human BT 474 cells is described. Also described are single exon nucleic acid probes expressed in the BT 474 cells and their use in methods for detecting gene expression.

WO 01/57271 A2